

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 10, 2002, 10:53:06 ; Search time 40.93 Seconds  
(without alignments)  
1072.116 Million cell updates/sec

Title: US-09-280-567-2  
Perfect score: 1634  
Sequence: 1 MRALEGSLSLCLVLALPA.....RVARMPGLERSVRERFLPVH 300

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL.17.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1634	100.0	300	4	O95407
2	444	27.2	401	4	O00300
3	440.5	27.0	372	4	Q9UHP4
4	425.5	26.0	401	11	O08727
5	424.5	26.0	401	11	O08712
6	395	24.2	302	13	Q9PUS0
7	338.5	20.7	425	4	Q16042
8	333.5	20.4	459	11	Q62327
9	327	20.0	482	11	O88734
10	297	18.2	630	13	Q98SM6
11	291.5	17.8	655	11	Q9EPU5
12	287	17.6	655	4	O75509
13	282.5	17.3	348	12	O57277
14	280.5	17.2	348	12	O57103
15	280.5	17.2	348	12	O57108
16	276	16.9	349	12	O57100
17	274	16.8	349	12	O57291
18	274	16.8	349	12	O57101
19	274	16.8	349	12	O57102

20	273	16.7	349	12	O57099	O57099 monkeypox v
21	265	16.2	350	12	O57116	O57116 cowpox viru
22	264.5	16.2	355	12	O85308	O85308 cowpox viru
23	262.5	16.1	349	12	O57110	O57110 variola vir
24	262.5	16.1	349	12	O57111	O57111 variola vir
25	262.5	16.1	349	12	O89118	O89118 variola vir
26	262.5	16.1	349	12	O89098	O89098 variola vir
27	262	16.0	348	12	O57112	O57112 variola vir
28	262	16.0	348	12	O85407	O85407 variola vir
29	261.5	16.0	349	12	O57284	O57284 camelpox vi
30	261.5	16.0	349	12	O57098	O57098 camelpox vi
31	259.5	15.9	349	12	O57305	O57305 cowpox viru
32	259.5	15.9	360	12	O57118	O57118 cowpox viru
33	258.5	15.8	351	12	O57117	O57117 cowpox viru
34	258.5	15.8	351	12	O73559	O73559 cowpox viru
35	257.5	15.8	326	12	O57120	O57120 cowpox viru
36	257.5	15.8	349	12	O57097	O57097 camelpox vi
37	254.5	15.6	326	12	O57122	O57122 cowpox viru
38	254.5	15.6	349	12	O57109	O57109 variola vir
39	253.5	15.5	347	12	O57115	O57115 cowpox viru
40	251.5	15.4	347	12	O57119	O57119 cowpox viru
41	250.5	15.3	351	12	O57121	O57121 cowpox viru
42	249	15.2	283	6	Q9XSZ8	Q9XSZ8 cercopithec
43	245.5	15.0	350	12	O57123	O57123 cowpox viru
44	239	14.6	616	4	Q9Y6Q6	Q9Y6Q6 homo sapien
45	233.5	14.3	625	11	O35305	O35305 mus musculu

## ALIGNMENTS

RESULT	1
O95407	
ID	O95407
AC	O95407; PRELIMINARY; PRT; 300 AA.
DT	01-MAY-1999 (TrEMBLrel. 10, Created)
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE	DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1).
GN	DCR3 OR TR6 OR TNFRSF6B.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID:9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=99087336; PubMed=9872321;
RA	Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA	Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA	Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA	Goddard A.D., Botstein D., Ashkenazi A.;
RT	"Genomic amplification of a decoy receptor for Fas ligand in lung and
RT	colon cancer.";
RL	Nature 396:699-703(1998).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BLOOD;
RX	MEDLINE=99253915; PubMed=10318773;
RA	Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT	"A newly identified member of tumor necrosis factor receptor
RT	superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL	J. Biol. Chem. 274:13733-13736(1999).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=PANCREAS;
RX	MEDLINE=20122600; PubMed=10655513;
RA	Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA	Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.F.;
RT	"Overexpression of M68/DCR3 in human gastrointestinal tract tumors
RT	independent of gene amplification and its location in a four-gene
RT	cluster.";
RL	Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN	[4]

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RP SEQUENCE FROM N.A.
RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF104419; AAD03056.1; -
DR EMBL; AF134240; AAD29688.1; -
DR EMBL; AF211779; AAF35244.1; -
DR EMBL; AF211793; AAF33685.1; -
DR EMBL; AF211794; AAF33686.1; -
DR EMBL; AF211845; CAC03668.1; -
DR HSP; P25942; ICDF.
DR InterPro: IPR000501; EGF-like.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 4.
DR ProDom: PD000771; TNFR_C6; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS00550; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 300 AA; 32679 MW; F90AEE33718449AF CRC64;

Query Match 100.0%; Score 1634; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 6.4e-139;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 1 MRALEGGSLLLCLVLPVPAVGVGVAETPTVPRDAETGERLVCAQCPTGVQV 60
Db 1 MRALEGGSLLLCLVLPVPAVGVGVAETPTVPRDAETGERLVCAQCPTGVQV 60
QY 61 PCRRDPTTCGPPRRHYTFQWNYLCRCVNVLCGEREEERACHATHNRACRRTGFF 120
Db 61 PCRRDPTTCGPPRRHYTFQWNYLCRCVNVLCGEREEERACHATHNRACRRTGFF 120
QY 121 AHAGFLEHASCPPGAGVIAPGTPSNTQCPGPTGTFSSSSSCQCPHNRCTALGLA 180
Db 121 AHAGFLEHASCPPGAGVIAPGTPSNTQCPGPTGTFSSSSSCQCPHNRCTALGLA 180
QY 181 LNVPGSSSHDTCTCTGTPPLSTRVPGAECERAVIDFAQDISIKRLQLLQALEAPE 240
Db 181 LNVPGSSSHDTCTCTGTPPLSTRVPGAECERAVIDFAQDISIKRLQLLQALEAPE 240
QY 241 GWGPTPRAGRAALQLKRLRLTELLGAQDQALLVRLQLALVARMFGLERSVRELPVH 300
Db 241 GWGPTPRAGRAALQLKRLRLTELLGAQDQALLVRLQLALVARMFGLERSVRELPVH 300

RESULT 2
OO0300 PRELIMINARY; PRT; 401 AA.
AC OO0300; O60236;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE OSTEOPTERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97262071; PubMed=9108485;
RX Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.";

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RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG FIBROBLAST;
RX MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
osteoclastogenesis in vitro.";
RL Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL Eur. J. Biochem. 254:685-691(1998).
CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
SIMILARITY).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN
THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; AB002146; BAA25910.1; -.
DR EMBL; AB008822; BAA32076.1; -.
DR EMBL; AB008821; BAA32076.1; JOINED.
DR HSP; P25942; ICDF.
DR MIM: 602643; -.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 3.
DR ProDom: PD000771; TNFR_C6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS00550; TNFR_NGFR_2; 2.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 401 OSTEOPTERIN.
FT DOMAIN 23 183 4 X TNFR-CYS.
FT REPEAT 23 63 TNFR-CYS 1.
FT REPEAT 64 106 TNFR-CYS 2.
FT REPEAT 107 143 TNFR-CYS 3.
FT REPEAT 144 201 TNFR-CYS 4.
FT DOMAIN 306 365 DEATH DOMAIN.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 87 105 BY SIMILARITY.
FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 263 263 A -> D (IN REF. 2 AND 3).
SQ SEQUENCE 401 AA; 45996 MW; EB42FA51C9D7C71E CRC64;

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Query Match

27.2%; Score 444; DB 4; Length 401;

Query Match 26.0%; Score 425.5; DB 11; Length 401;  
Best Local Similarity 39.5%; Pred. NO. 2.6e-30;  
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;

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QY 34 PTYPWRDAETGERLVAQCPPTGTFVQPCRRDSTTCGCPGPPRHRYTQFWNYLRCRYCNV 93
DB 26 PKYLHVDPTGTHQLLCKDKAPGYLKHQCTVRRKTLCLVPCPDYSYDSWHTSDCVYCSP 85
QY 94 LCGEREEARACHATHNACRRCRTGTFFAHAGFCLEHASCPGAGVIAPGTPSNTQCPC 153
DB 86 VKCELTVQKECNRTHNRVCEEGRYLEFCLKHKRSCPPGLGVLOAGTPERTVCKRC 145
QY 154 PCGTFSASSSSQCPHRCNCTALGALNVPVSSSHDTCTCTGFPPLSTRVPGAE--C 211
DB 146 PDGFFSGETSSKAPCRKHNCSLSGLLLIOKGNATHDNV---CSGNREATQCGIDVTL 202
QY 212 ERAVIDFAFQDISIKRLQRLQAL 236
DB 203 EEAFFFAVPTKIIPNWSLVLDL 227

RESULT 5
ID 008712 PRELIMINARY; PRT; 401 AA.
AC 008712; 070202;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE OSTROPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
DE (OCIF).
GN TNFRSF11B OR OPG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=KIDNEY;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trill G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/OLA, AND NIH SWISS;
RX MEDLINE=98382527; PubMed=9714833;
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
RA Higashio K.;
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
RT gene and its expression in embryogenesis.";
RL Gene 215:339-343(1998).
CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
CC PLACENTA. NOT DETECTED IN SPLEEN.
CC -!- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
CC 15 TO DAY 17.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DB EMBL; 094331; AA853708.1;
DB EMBL; AB013896; BAA28269.1;
DB EMBL; AB013903; BAA33388.1;
DB EMBL; AB013899; BAA33388.1; JOINED.
DB EMBL; AB013900; BAA33388.1; JOINED.
DB EMBL; AB013901; BAA33388.1; JOINED.
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DR EMBL; AB013902; BAA33388.1; JOINED.
DR HSSP; P25942; 1CDF.
DR MGD; MGI:109587; Tnfrsf11b.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001388; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR ProDom; PD000771; TNFR_C6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Glycoprotein; Repeat; Cytokine; Signal.
FT SIGNAL 1 21 OSTEOPROTEGERIN.
FT CHAIN 22 401 4 X TNFR-CYS.
FT DOMAIN 23 201
FT REPEAT 23 63 TNFR-CYS 1.
FT REPEAT 23 63 TNFR-CYS 2.
FT REPEAT 64 106 TNFR-CYS 3.
FT REPEAT 107 143 TNFR-CYS 3.
FT REPEAT 144 201 TNFR-CYS 4.
FT DOMAIN 306 365 DEATH DOMAIN.
FT DISULFID 41 54 BY SIMILARITY.
FT DISULFID 44 62 BY SIMILARITY.
FT DISULFID 65 80 BY SIMILARITY.
FT DISULFID 83 97 BY SIMILARITY.
FT DISULFID 87 105 BY SIMILARITY.
FT DISULFID 118 142 BY SIMILARITY.
FT DISULFID 145 160 BY SIMILARITY.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH
FT SWISS).
FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH
FT SWISS).
FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH
FT SWISS).
FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH
FT SWISS).
FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH
FT SWISS).
FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 26.0%; Score 424.5; DB 11; Length 401;
Best Local Similarity 39.0%; Pred. No. 3.2e-30;
Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;

QY 34 PTYPWRDAETGERLVAQCPPTGTFVQPCRRDSTTCGCPGPPRHRYTQFWNYLRCRYCNV 93
DB 26 PKYLHVDPTGTHQLLCKDKAPGYLKHQCTVRRKTLCLVPCPDYSYDSWHTSDCVYCSP 85
QY 94 LCGEREEARACHATHNACRRCRTGTFFAHAGFCLEHASCPGAGVIAPGTPSNTQCPC 153
DB 86 VKCELTVQKECNRTHNRVCEEGRYLEFCLKHKRSCPPGLGVLOAGTPERTVCKRC 145
QY 154 PCGTFSASSSSQCPHRCNCTALGALNVPVSSSHDTCTCTGFPPLSTRVPGAE--C 211
DB 146 PDGFFSGETSSKAPCRKHNCSLSGLLLIOKGNATHDNV---CSGNREATQCGIDVTL 202
QY 212 ERAVIDFAFQDISIKRLQRLQAL 236
DB 203 EEAFFFAVPTKIIPNWSLVLDL 227

RESULT 6
QYPU50 PRELIMINARY; PRT; 302 AA.
ID Q9PUS0
AC Q9PUS0
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
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DR	PROSITE; PS00652; TNFR_NGFR_1; 1.
DR	PROSITE; PS00500; TNFR_NGFR_2; 3.
KW	Receptor.
FT	NON_TER
SQ	SEQUENCE 425 AA; 44608 MW; 1B24A97E3AD4CF9F CRC64;
Query Match 20.7%; Score 338.5; DB 4; Length 425;	
Best Local Similarity 30.1%; Pred. No. 1.8e-22;	
Matches 82; Conservative 43; Mismatches 110; Indels 37; Gaps	
Qy	46 RLVCACQPPGTFVQRCRDSPTTCGCPPRHHYTFQWNYLERCRYCNVLCGBEEBEEARAC 105
Db	15 QMCCSKCSPGOHAKVFCTKTSDTVCDSCESTDTQLWNWVPECLSCGRCSSDOVETQAC 74
Qy	106 HATNRCACRTGFFAHAG-----FCLERHASCPPGAGVIAPGTPSONTCQCPCPPGTFES 159
Db	75 TREONRICTCPGWYCALSKQEGCRICAPLKRCPGFGVARGPTETSDVVCKPCAPGTFES 134
Qy	160 ASSSSQEQPHRNCTALGALANVPGSSSHDTLCTSGTGPLSTRVPGAEECERAVIDFV 219
Db	135 NTTSTSDICRPHQICNVVA---IPGNASMDAVCTSTS---PTRSMAPGAVHLPQPV--- 184
Qy	220 AFQDISIKRLQRLQALEAPE-----GWGTPRA-----GRAALQKLRLRLTELLGAQDG 270
Db	185 ---STRSQHTQPTPEPSTAPSTSFLLPMGSPPAEGSTGDFALPVLGVGVTAAL-----G 236
Qy	271 ALLVRLQLAL---RVARMP-GLERSVREFLP 298
Db	237 LLIIGVVNCVIMTQVKKKPLCLOREAKVPHLP 268
RESULT 8	
Q62327	PRELIMINARY; PRT; 459 AA.
AC Q62327;	
DT 01-NOV-1996 (Tremblrel. 01, Created)	
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)	
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)	
DE TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).	
OS Mus musculus (Mouse)	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX NCBI_TaxId=10090;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=ND;	
RA MEDLINE=95I78848; PubMed=7873884;	
DR HSP; P19438; INCF.	
DR InterPro; IPR001368; TNFR_c6.	
DR Pfam; PF00020; TNFR_c6; 4.	
DR ProDom; PD000771; TNFR_c6; 1.	
DR SMART; SM00208; TNFR; 4.	
DR PROSITE; PS00652; TNFR_NGFR_1; 2.	
DR PROSITE; PS00500; TNFR_NGFR_2; 3.	
FT NON_TER 1	
FT VARIANT 87 87 S -> T.	
FT VARIANT 93 93 T -> I.	
FT VARIANT 268 268 F -> I.	
FT VARIANT 345 345 S -> F.	
FT VARIANT 421 421 Y -> C.	
SQ SEQUENCE 459 AA; 44866 MW; 6C51D2CF1C4626DF CRC64;	
Query Match 20.4%; Score 333.5; DB 11; Length 459;	
Best Local Similarity 29.7%; Pred. No. 5.3e-22;	
Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps	

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QY 46 RLVCACPGTGVQVRCRDRDPTTCGCPPRHYTQFWNYLRCRYCNVLCGEREEARAC 105
DB 37 QMCCAKPPGQYVKHCNKTSDTVACDCEASMYTQVWNOFRTCLSCSSCSTDQVETRAC 96
QY 106 HATHNACRCRTGFF---AHAGF---CLEHASCPPGAGVIAPGTPSNTQCPGPGTF 158
DB 97 TKOONRVACACEAGRYCALKTHSGSCRCQMLSKCGFGVASSRAPNGNVLCACAPGTF 156
QY 159 SASSSECOQPHRNCNTALGLNVPSSSHDTLCT---SCTGFPLSTRVPGABECERA 214
DB 157 SDTSTSDVCRPHRCSILA---IFGNASTDAVCAPESTLSAIPRTLYVSQPEPTRSQ 212
QY 215 VIDFAQDISIKRLQRLQALQALPEGWGTP-----RAGRAALQKLRRRLTELGAQD 269
DB 213 PLD-----QEPGSPQTSILTSL-----GSTPIEQSTKGGISLPIGLVGTSL----- 257
QY 270 GALLVRLQAL-----RVARMPGLERSVRERFLP 298
DB 258 GLMLGLVNCFILVQKKPKSCLQORDAKVPHVP 290

RESULT 9
ID O88734 PRELIMINARY; PRT; 482 AA.
AC O88734;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE P80 TNF-ALPHA RECEPTOR.
GN TNFR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hurlie B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT "The Mouse Tumor Necrosis Factor Receptor Gene:Genomic Structure and
Characterization of the two Transcripts.";
RL Genomics 0:0-0(0).
DR EMBL; Y14619; CAAT4969.1; JOINED.
DR EMBL; Y14620; CAAT4969.1; JOINED.
DR EMBL; Y14621; CAAT4969.1; JOINED.
DR EMBL; Y14622; CAAT4969.1; JOINED.
DR EMBL; Y14623; CAAT4969.1; JOINED.
DR EMBL; Y14679; CAAT4969.1; JOINED.
DR HSSP; PI9438; INCF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FF83C CRC64;

Query Match 20.0%; Score 327; DB 11; Length 482;
Best Local Similarity 29.3%; Pred. No. 2.1e-21;
Matches 82; Conservative 43; Mismatches 109; Indels 46; Gaps 10;

QY 46 RLVCACPGTGVQVRCRDRDPTTCGCPPRHYTQFWNYLRCRYCNVLCGEREEARAC 98
DB 52 QMCCAKPPGQYVKHCNKTSDTVACDCEASMYTQVWNOFRTCLSCSSCSTDQVETRAC 111
QY 99 EEEARACHATHNRCRCRTGFF---AHAGF---CLEHASCPPGAGVIAPGTPSNTQCOQ 151
DB 112 QVETRACTQQNRVACACEAGRYCALKTHSGSCRCQMLSKCGFGVASSRAPNGNVLCCK 171
QY 152 PCPPPTGSSSSSSCOQPHRNCNTALGLNVPSSSHDTLCT---SCTGFPLSTRVPG 207
DB 172 ACAPGTFSTSDTVCRPHRCSILA---IPGNASTDAVCAPESTLSAIPRTLYVSQ 227
QY 208 ABECERAVIDFAVFQDISIKRLQRLQALQALPEGWGTP-----RAGRAALQKLRRRLT 262
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DB 228 PEPTRSQPLD---QEPGSPQTSILTSL-----GSTPIEQSTKGGISLPIGLVGT 277
QY 263 ELLGADQDGLLYRLQAL-----RVARMPGLERSVRERFLP 298
DB 278 SL-----GLMLGLVNCFILVQKKPKSCLQORDAKVPHVP 312

RESULT 10
ID Q98SM6 PRELIMINARY; PRT; 630 AA.
AC Q98SM6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DEATH RECEPTOR 6 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgham J.T., Johnson A.L.;
RT "Expression of DR6 in the ovary.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349908; AAK29666.1; -.
KW Receptor.
FT NON_TER.
SQ SEQUENCE 630 AA; 68977 MW; 53C53BD1C4B25567 CRC64;

Query Match 18.2%; Score 297; DB 13; Length 630;
Best Local Similarity 34.2%; Pred. No. 1.4e-18;
Matches 55; Conservative 27; Mismatches 79; Indels 0; Gaps 0;

QY 40 DAETGERLVACACPGTGVQVRCRDRDPTTCGCPPRHYTQFWNYLRCRYCNVLCGERE 99
DB 22 DRATNOELICDKCPAGTYVSKHCTKSTLRCSGPCDGTFTKHENGIERCHCRKPCPLM 81
QY 100 EEARACHATHNRCRCRTGFFAHAGFCLHASCPCGAGVIAPGTPSNTQCOQCPGTF 159
DB 82 IERTHTALTDRCTCLSGTFQINDTCVPTVCPVGVKRGKTETEDVRCKPCPRGTF 141
QY 160 ASSSSECOQPHRNCNTALGLNVPSSSHDTLCTCTCTGFP 200
DB 142 DVPSSVMKCKTYTDCFGKNNVVVKPGTKESDNCVCGSPASLP 182

RESULT 11
ID Q9EPU5 PRELIMINARY; PRT; 655 AA.
AC Q9EPU5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=KIDNEY;
RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA Minami M.;
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
(DR6).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF322069; AAG38115.1; -.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
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KW Receptor.
SQ SEQUENCE 655 AA; 71844 MW; 489393991C4852A33 CRC64;

Query Match 17.6%; Score 287; DB 4; Length 655;
Best Local Similarity 34.3%; Pred. No. 11e-17;
Matches 58; Conservative 23; Mismatches 88; Indels 0; Gaps 0;

Qy 35 TYPRDRAETGRLVCAQCPGCTFVORCRRDSDPTTCGCPPPRHVTQFWNYLERCRYCNVL 94
|| || || || || || || || || || || || || || || || || || || || ||
Db 53 TYRHVDRTATGVLTCDCPKAGTYVYSEHCTNFTSLRVSSCPVGTFTRHENGIEKCHDCSQP 112
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Qy 95 CGEREERARACHATHNACRCRTCFEAFHAGFCLRHASCPCGAGVIAPCTPSONTCQPCP 154
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Db 113 CPWFMIKELPCAALTDRCTCPGFMFOSNATCAPTHVCPVGWGVKKGTETDVRCKQCA 172
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Qy 155 PGTFSSASSSEQCPHRNCTALGALNVPGSSSHDTLCTSCTGFPLST 203
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Db 173 RGTESDPSSVMKCKAYTDCLSLQNLVVIKPGTKETDNNVCGTLPFSFSST 221
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RESULT 13
O57277 PRELIMINARY; PRT; 348 AA.
AC O57277;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.

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RESULT 14

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057103
ID O57103 PRELIMINARY; PRT; 348 AA.
AC O57103;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ZAIRE-1970 (79-0005);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87847; AB94364.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
SQ SEQUENCE 348 AA; 38184 MW; 34A5E668B27907B5 CRC64;

Query Match 17.2%; Score 280.5; DB 12; Length 348;
Best Local Similarity 30.4%; Pred. No. 2.3e-17;
Matches 63; Conservative 34; Mismatches 97; Indels 13; Gaps 3;

QY 9 LSLLLCLVLPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPCPGTFVQRPCCRDSPT 68
DB 10 LFLSCLIIINGRDIAHAPNSGKCKDNEYRSN-----LCCLSCPPTGYASRLCDSKNT 63
QY 69 TCGPCPPRHYYTFWNYLRCRYCNVLCGEREEEARACHATHNRACRCRTGFF-----AH 122
DB 64 OCTPCGSDTFTSHNNHQAQLSCNGRCDNQVETRSCNTTHNRICECSPGYYCLLKSSG 123
QY 123 AGFCLEHASCPCGAGVIAPGTPSONTQOCPCPGTFSASSSSSEOCQPHRNCALGLALN 182
DB 124 CRTICSKTKCGIGYGV-SGYTSTGDVICSPCGPGTYSHTVSSDCKEPTVTSNTFNVIDVE 182
QY 183 VPGSSSHDTLCTSCGFPPLSTRVPGAE 209
DB 183 INLYPVNDTSCRTTTTGLSESISTSE 209

Search completed: May 10, 2002, 10:59:02
Job time: 356 sec
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057108
ID O57108 PRELIMINARY; PRT; 348 AA.
AC O57108;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ZAIRE-1970 (CONGO-8);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AB94367.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.

Query Match 17.2%; Score 280.5; DB 12; Length 348;
Best Local Similarity 30.4%; Pred. No. 2.3e-17;
Matches 63; Conservative 34; Mismatches 97; Indels 13; Gaps 3;

QY 9 LSLLLCLVLPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPCPGTFVQRPCCRDSPT 68
DB 10 LFLSCLIIINGRDIAHAPNSGKCKDNEYRSN-----LCCLSCPPTGYASRLCDSKNT 63
QY 69 TCGPCPPRHYYTFWNYLRCRYCNVLCGEREEEARACHATHNRACRCRTGFF-----AH 122
DB 64 OCTPCGSDTFTSHNNHQAQLSCNGRCDNQVETRSCNTTHNRICECSPGYYCLLKSSG 123
QY 123 AGFCLEHASCPCGAGVIAPGTPSONTQOCPCPGTFSASSSSSEOCQPHRNCALGLALN 182
DB 124 CRTICSKTKCGIGYGV-SGYTSTGDVICSPCGPGTYSHTVSSDCKEPTVTSNTFNVIDVE 182
QY 183 VPGSSSHDTLCTSCGFPPLSTRVPGAE 209
DB 183 INLYPVNDTSCRTTTTGLSESISTSE 209

RESULT 15
057108
ID O57108 PRELIMINARY; PRT; 348 AA.
AC O57108;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ZAIRE-1970 (CONGO-8);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AB94367.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
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OM protein - protein search, using sw model

Run on: May 10, 2002, 10:53:51 ; Search time 15.03 Seconds  
(without alignments)  
731.833 Million cell updates/sec

Title: US-09-280-567-2  
Perfect score: 1634  
Sequence: 1 MRALEGPLSLGLVLPALPA.....RVARMPGLERSVRERFLPVH 300

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	353.5	21.6	461	1	TNR2_HUMAN
2	332.5	20.3	474	1	TNR2_MOUSE
3	315	19.3	435	1	TNR2_HUMAN
4	277	17.0	415	1	TNR2_MOUSE
5	262.5	16.1	349	1	VC22_YARV
6	246	15.1	283	1	TR14_HUMAN
7	236.5	14.5	325	1	VT2_SFVKA
8	226	13.8	277	1	OX40_HUMAN
9	215	13.2	326	1	VT2_MXVL
10	214	13.1	271	1	OX40_RAT
11	211	12.9	277	1	CD40_HUMAN
12	203	12.4	289	1	CD40_MOUSE
13	202	12.4	269	1	CD40_BOVIN
14	198.5	12.1	272	1	OX40_MOUSE
15	186.5	11.4	595	1	CD30_HUMAN
16	185	11.3	256	1	41BB_MOUSE
17	176	10.8	416	1	NGFR_CHICK
18	175.5	10.7	427	1	NGFR_HUMAN
19	174	10.6	255	1	41BB_HUMAN
20	170	10.4	425	1	NGFR_RAT
21	163	10.0	332	1	FASA_PIG
22	160.5	9.8	471	1	TNR1_BOVIN
23	155.5	9.5	260	1	CD27_HUMAN
24	155.5	9.5	327	1	FASA_MOUSE
25	155	9.5	323	1	FASA_BOVIN
26	153	9.4	241	1	TR18_HUMAN
27	148	9.1	250	1	CD27_MOUSE
28	147.5	9.0	5376	1	ZAN_MOUSE
29	145	8.9	335	1	FASA_HUMAN
30	144	8.8	324	1	FASA_RAT
31	137.5	8.4	454	1	TNR1_MOUSE
32	129.5	7.9	1877	1	PKC5_MOUSE
33	128.5	7.9	417	1	WSL1_HUMAN

34	128.5	7.9	3635	1	LMA5_MOUSE
35	127	7.8	1192	1	LMA2_MOUSE
36	125.5	7.7	461	1	TNR1_RAT
37	125.5	7.7	1255	1	ERB2_HUMAN
38	124.5	7.6	1696	1	PKC5_BRACL
39	124.5	7.6	1713	1	LMA3_HUMAN
40	124.5	7.6	3106	1	LMA2_MOUSE
41	123.5	7.6	455	1	TNR1_HUMAN
42	123.5	7.6	2813	1	VWF_CANFA
43	123	7.5	2569	1	LMA3_MOUSE
44	120	7.3	1609	1	LMG1_HUMAN
45	120	7.3	2318	1	NTC3_MOUSE

## ALIGNMENTS

RESULT	1
TNR2_HUMAN	
ID	TNR2_HUMAN
AC	P20333; STANDARD; PRT; 461 AA.
DT	01-FEB-1991 (Rel. 17, Created)
DT	01-AUG-1991 (Rel. 19, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).
DE	TNFRSF1B OR TNFR2 OR TNFR.
GN	Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=90260639; PubMed=2160731;
RA	Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R., Dower S.K., Cosman D., Goodwin R.G.;
RT	"A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins.";
RT	Science 248:1019-1023(1990).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91045991; PubMed=2172983;
RA	Kohn T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W., Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT	"A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor.";
RT	Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96299745; PubMed=8661109;
RA	Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J., Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J., Brodeur G.M.;
RT	"Physical mapping and genomic structure of the human TNFR2 gene.";
RT	Genomics 35:94-100(1996).
RN	[4]
RP	SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
RX	MEDLINE=90349572; PubMed=2166946;
RA	Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D., Ringold G.M.;
RT	"Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor.";
RT	Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN	[5]
RP	SEQUENCE OF 27-31.
RX	MEDLINE=90110215; PubMed=2153136;
RA	Engelmann H., Novick D., Wallach D.;
RT	"Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.";
RT	J. Biol. Chem. 265:1531-1536(1990).
RN	[6]
RP	SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.

RX MEDLINE=91056048; PubMed=2173696;  
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
 RA Brockhaus M.;  
 RT "Purification and partial amino acid sequence analysis of two  
 RT distinct tumor necrosis factor receptors from HL60 cells.";  
 RL J. Biol. Chem. 265:20131-20138(1990).  
 RP [7]  
 RP CHARACTERIZATION.  
 RX MEDLINE=93016040; PubMed=1328224;  
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
 RA Lipari M.T., Goeddel D.V.;  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
 RT Characterization of ligand binding, internalization, and receptor  
 RT phosphorylation.";  
 RL J. Biol. Chem. 267:21172-21178(1992).  
 RN [8]  
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.  
 RX MEDLINE=99221490; PubMed=10206649;  
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 RT "Structural basis for self-association and receptor recognition of  
 RT human TRAF2.";  
 RL Nature 398:533-538(1999).  
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND  
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW  
 CC LEVEL ON THREONINE RESIDUES.  
 CG -!- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND  
 CC WYETH-AYERST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID  
 CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING  
 CC PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO  
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -!- DATABASE: NAME-PROW: NOTE-CD guide CD120b entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".  
 CC -!- DATABASE: NAME-Enbrel; NOTE-Clinical information on Enbrel;  
 CC WWW="http://www.enbrelinfo.com/".  
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 CC -----  
 DR EMBL; M32315; AAC59929.1; -;  
 DR EMBL; M35057; AAC63262.1; -;  
 DR EMBL; U52165; AAC50622.1; -;  
 DR EMBL; U52156; AAC50622.1; JOINED.  
 DR EMBL; U52157; AAC50622.1; JOINED.  
 DR EMBL; U52158; AAC50622.1; JOINED.  
 DR EMBL; U52159; AAC50622.1; JOINED.  
 DR EMBL; U52160; AAC50622.1; JOINED.  
 DR EMBL; U52161; AAC50622.1; JOINED.  
 DR EMBL; U52162; AAC50622.1; JOINED.  
 DR EMBL; U52163; AAC50622.1; JOINED.  
 DR EMBL; U52164; AAC50622.1; JOINED.  
 DR EMBL; M55994; AAC36755.1; -;  
 DR PIR; A35356; A35356.  
 DR PIR; A36007; A36007.  
 DR PIR; A36475; A36475.  
 DR PIR; B35010; B35010.  
 DR PIR; A23666; A23666.  
 DR PDB; 1CA9; 12-APR-99.  
 DR MIM; 191191; -;  
 DR InterPro; IP0001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR ProDom; PD000771; TNFR\_c6; 1.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR.1; 2.  
 DR PROSITE; PS00652; TNFR\_NGFR.2; 4.  
 \*W Receptor; Transmembrane; Glycoprotein; Repeat; Signal;

KW Phosphorylation; Pharmaceutical; 3D-structure.  
 FT SIGNAL 1 22  
 FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.  
 FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 258 287 POTENTIAL.  
 FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 39 201 4 X TNFR-CYS.  
 FT REPEAT 39 76 TNFR-CYS 1.  
 FT REPEAT 77 118 TNFR-CYS 2.  
 FT REPEAT 119 162 TNFR-CYS 3.  
 FT REPEAT 163 201 TNFR-CYS 4.  
 FT DISULFID 40 53 BY SIMILARITY.  
 FT DISULFID 54 67 BY SIMILARITY.  
 FT DISULFID 57 75 BY SIMILARITY.  
 FT DISULFID 78 93 BY SIMILARITY.  
 FT DISULFID 96 110 BY SIMILARITY.  
 FT DISULFID 100 118 BY SIMILARITY.  
 FT DISULFID 120 126 BY SIMILARITY.  
 FT DISULFID 134 143 BY SIMILARITY.  
 FT DISULFID 137 161 BY SIMILARITY.  
 FT DISULFID 164 179 BY SIMILARITY.  
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 141 141 R -> P (IN REF. 4).  
 FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).  
 FT CONFLICT 363 363 A -> T (IN REF. 4).  
 SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;  
  
 Query Match 21.6%; Score 353.5; DB 1; Length 461;  
 Best Local Similarity 29.8%; Pred. No. 1.1e-20;  
 Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;  
  
 QY 8 GLSLCLVLALPALLPVPVAVRGVAETPTYPWRDAEAGE-----RLVCAQCPCPG 55  
 DB 13 GLELWAAHALPA-----QVAFTPYAP----EPGTCRLREYDYDTAQMCCKSCSPG 60  
  
 QY 56 TFVQRCRRDSPTTCPCPRHYTFQWNYLERCRYCNVLCGEREEARACHATHNACRC 115  
 DB 61 QHAKVCTCTSDTVDCSDCEDSYITQLWNVPECLSCGRCSSDOVETQACTRQNRICTC 120  
  
 QY 116 RTGFFAHAG-----FCLSHASCPGAGVIAPTQSPQTCQCPPTGTSASSSSSEQC 169  
 DB 121 RFGWYCALSKQEGCRCLKRCRPGFVGARPGTETSDVVKPCAPGTFSTNTSSTDICR 180  
  
 QY 170 PHRNCTALGALNVPGSSSHDITCTSCGFLPLSTRYPGAECECERAVIDFVAFQDISIKRL 229  
 DB 181 PHQICNVVA-----IPGNASRDVACTSTS--PTRSMAPGAVHLPQPV-----STRSQHT 227  
  
 QY 230 QRLQLQALEAPE-----GWGPTPRA-----GRAALQLKRLRRLTELLGAQDQALVRLQAL 280  
 DB 228 QQTPEPSTAPSTSFLLPMGFPSPGEGSTGDFALPGLVGVITAL-----GLLIIGVNVCV 282  
  
 QY 281 ----RVARMP-GLERSVREFLP 298  
 DB 283 IMTVQKKKPLCLQREAKVPHLP 304  
  
 RESULT 2  
 ID TNFR2\_MOUSE STANDARD; PRT; 474 AA.  
 AC P25119; P97893;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).  
 OS TNFRSF1B OR TNFR2 OR TNFR-2.  
 GN Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

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SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 20.3%; Score 332.5; DB 1; Length 474;
Best Local Similarity 29.7%; Pred No 4.8e-19;
Matches 81; Conservative 44; Mismatches 109; Indels 39; Gaps 9;

QY 46 RLVAQCPPGTGVQRCRRSDPTTCGPPRRHYTFWNLYLRCRYCNVLGEEEEARAC 105
   : : ||||| : : : : ||||| : : : : ||||| : : : : |||||
Db 52 QMCCACPPGGYVYKHCNKTSDTVCADCEASMYTVWVNOFTCLSCSSCTTDOVEIRAC 111

QY 106 HATHNACRCRTGFF-----AHAGF---CLEHASCPGAGVYTAGTPSONTOCQPCPGTF 158
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 112 TKQGNRYCACEAGRYCALKTHSGSCRCMRLSKCGPGFGVASSRPNAGNVLCACPGTF 171

QY 159 SASSSSQEQPHRNCNTALGLNALNVPSSSHDITLCT---SCTGFPLSTRVPGAECECERA 214
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 SDTSSSDVCRPHRISCSILA-----IPGNASTDAVCAPESPTLSAIPRTLYYSQPEPTRSQ 227

QY 215 VIDFVAFQDISIKRLQLQALEAPEGWGPTP-----RAGRAALQLKRLRRITELLGAQD 269
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 PLD---QEPGCSQTPSILASL-----GSTPIIEQSTKGGISLPIGLIVGVTSL----- 272

QY 270 GALLVRLQAL-----RVAMPGLERSVRERFLP 298
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 273 GLLMGLVNGVLCILVORKKKPKSCLOQDAKVHPV 305

RESULT 3
TNRG_HUMAN STANDARD; PRT; 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN LTBFR OR TNFRSF3 OR TNFRSF3F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; Pubmed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human l2p
RT transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
RN [2]
RS FUNCTION
RP MEDLINE=94225209; Pubmed=8171323;
RX Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC
CC EMBL; L04270; AAA36757.1;
CC HSSP; P25942; 1CDF.
CC MIM; 600979;

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DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00505; TNFR_NGFR_2; 3.
DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
KW SIGNAL 1 30
FT CHAIN 31 435
FT DOMAIN 31 227
FT TRANSMEM 228 248
FT DOMAIN 249 435
FT DOMAIN 42 211
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 168
FT REPEAT 169 211
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 148
FT DISULFID 142 167
FT DISULFID 170 185
FT CARBOHYD 40 40
FT CARBOHYD 177 177
SQ SEQUENCE 435 AA; 46709 MW; 62462656022656F CRC64;

Query Match 19.3%; Score 315; DB 1; Length 435;
Best Local Similarity 31.8%; Pred. No. 1e-17;
Matches 89; Conservative 29; Mismatches 120; Indels 42; Gaps 12;

QY 3 ALEGGSLCLLVLPALPVPVAVGVAETPT-----PWRDA-----ETGERLVCAQC 52
Db 6 ATSAPGLAWPLVLGLFLGFLAASQPAV---PPYASENQTCDQKEYEYPQHRCSSRC 62
QY 53 PPGTFVQRCRDSPTTCGPPRHYTFQFNWYL---EERCYNVLCGEREEARACHATH 109
Db 63 PPGTFVSAKSRIDTVCAENSYNEHNYLTICQLCRPCDPVWG---LEEIAPTCKR 120
QY 110 NRACRRTGFFAHAGFLE-H-----ASCPGGA-GVIAPGTPSQNTQCQPPGTFSSASS 162
Db 121 KTCRCQCPMFC-AAWALECTHCELLSDCPCTEAEELKDEVGKGNHCVCKAGHFQNTS 179
QY 163 SSSEOCQPHRNTALGLALNVPSSSHDTLCTSCGFPPLSTRVPGAECECAVIDFVAFQ 222
Db 180 SPSARCQPHTRCENGLVEAPGTAQSDTCKNPLE-PLPPEMSGTMLMLAVLLPLAFL 238
QY 223 DIS-----IKRLQLQALEAPEGWTTPRAG 249
Db 239 LLATVFVSCIWKSHPSLCRLKGLSLK--RRPQEGPNPVAG 276

RESULT 4
TNRC_MOUSE
ID TNRC_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN LTBR OR TNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-CVB; TISSUE=Lung;
```

```
RX MEDLINE-96072804; PubMed-7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression.";
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-96163885; PubMed-8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping.";
RL Genomics 30:312-319(1995).
CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC -----
DR EMBL: U29173; AAA68964.1; -
DR EMBL: L38423; AAB00846.1; -
DR EMBL: U30798; AAB81334.1; -
DR HSSP: P25942; ICDF.
DR MGD; MGI:104875; Ltbr.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00505; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 415
FT DOMAIN 31 223
FT TRANSMEM 224 244
FT DOMAIN 245 415
FT DOMAIN 42 213
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 170
FT REPEAT 171 213
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 150
FT DISULFID 142 169
FT DISULFID 172 187
FT CARBOHYD 40 40
FT CARBOHYD 179 179
SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match 17.0%; Score 277; DB 1; Length 415;
Best Local Similarity 31.2%; Pred. No. 9.2e-15;
Matches 88; Conservative 29; Mismatches 105; Indels 60; Gaps 14;

QY 6 GP---GLSLCLLVLPALPVPVAVGVAETPTYPWRDAETGERL---VCAOCPGCTFVQ 59
Db 15 GPLLLGLSGL-LVASQPLVPPYRI-----ENOTCWDQDREYEPHMDVCCSPGGEFV 69
QY 60 RPCRDSPTTCGPPRHYTFQFNWYL---EERCYNVLCGEREEARACHATHNACRCR 116
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Db 70 AVCSRSQDVTCKTCPHNSNEHNNHLSTCOLCRPCDIVLG--FEVAPCTSDRKAECRCQ 127
QY 117 TGFFAHAGFLC-----EHCSPGAGVIA-PGTPSQNT-----OCQPCPGCTFSASSS 163
Db 128 PGM-----SCVLDNECVCEERLVLCQPGTEAEVTDIMDTDNCVCKFGHFONTSS 182
QY 164 SSEQCOPHNCRTALGIALNVPSSSHDTCTCTGTPPLSTRVPGAECEERAVIDFAV-- 221
Db 183 PRACQPHTRCEITQGLVEAPGTSYSDTICK-----NPPPGGAMLLAILLSLVLFLL 235
QY 222 -----QDISIKRLQRLQALAEPEGWG-----PTPRA 248
Db 236 FTTVLACAMWRHPSLCRKLGLTLK--RHPEGESPPCPAPRA 275

RESULT 5
VC22_VARV STANDARD; PRT; 349 AA.
AC P34015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 01-JUN-1994 (Rel. 29, Last annotation update)
DE PROTEIN C22/B28 HOMOLOG.
GN GAR.
OS Variola virus.
OC Viruses; GSDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-INDIA-1967 / ISOLATE IND3;
RX MEDLINE=93202281; PubMed=8394129;
RA Shchelkunov S.N., Bilinov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
CC -1- SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X69198; CAA49137.1; -
CC EMBL; X67117; CAA47540.1; -
CC PIR; D36858; D36858.
CC PIR; S35987; S35987.
CC PIR; S46888; S46888.
CC HSSP; P19438; INCF.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 2.
CC ProDom; PD000771; TNFR_c6; 1.
CC SMART; SM00208; TNFR; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC Repeat.
KW Repeat.
FT DOMAIN 31 108 2 X TNFR-CYS.
FT REPEAT 31 66 TNFR-CYS 1.
FT REPEAT 67 108 TNFR-CYS 2.
SQ SEQUENCE 349 AA; 38189 MW; D45D40B5C6E780EF CRC64;

Query Match 16.1%; Score 262.5; DB 1; Length 349;
Best Local Similarity 30.0%; Pred. No. 1.le-13;
Matches 62; Conservative 29; Mismatches 103; Indels 13; Gaps 3;
QY 9 LSLCLVLVALLPVPVAVGVAEPTTPWRDAETGERLVCAOCPPCTFVQRCRRDSPT 68
Db 10 LFLSCIIINGRDAAPTTPPGKCKDTEY-----KRHNLCCLSCPPGTYASRLCDKSKNT 63
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QY 69 TCGCPPRHYTOFWNYLERYCYNVLGGEREERARACHATHNRACRRTGFF-----AH 122
Db 64 QCTPCGSGTFTSRNNHLPACLSGCRGNSNQVETRSNTTTHNRICESPGYCLLKSSG 123
QY 123 AGCLEHASCPPGAGVIAPGTPSQNTQCQPCPGTFSASSSSSEOCOPHNCRTALGIALN 182
Db 124 CKAKVSQTKGIGYGV-SGHTSVGDVICSPCGFGTSHTVSSADKCEPVPNTFNFDVE 182
QY 183 VPGSSSHDTLCTCTGTPPLSTRVPGAE 209
Db 183 ITLYPVNDTSCRTTTTGLSESLTSE 209

RESULT 6
TRI4_HUMAN STANDARD; PRT; 283 AA.
ID TR14_HUMAN
AC Q92956; Q9UM65;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 14 PRECURSOR
DE (HERPESVIRUS ENTRY MEDIATOR) (TUMOR NECROSIS FACTOR RECEPTOR-LIKE 2)
DE (TR2).
GN TNFRSF14 OR HVEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix adenocarcinoma;
RX MEDLINE=97053782; PubMed=8898196;
RA Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
RT "Herpes simplex virus-1 entry into cells mediated by a novel member of
RT the TNF/NGF receptor family.";
RL Cell 87:427-436(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97306336; PubMed=9162061;
RA Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
RA Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
RA Porter T.G., Truneh A., Young P.R.;
RT "A newly identified member of the tumor necrosis factor receptor
RT superfamily with a wide tissue distribution and involvement in
RT lymphocyte activation.";
RL J. Biol. Chem. 272:14272-14276(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Cao X.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR TNFSF14. INVOLVED IN LYMPHOCYTE ACTIVATION.
CC PLAYS AN IMPORTANT ROLE IN HSV PATHOGENESIS BECAUSE IT ENHANCED
CC THE ENTRY OF SEVERAL WILDTYPE HSV STRAINS OF BOTH SEROTYPES INTO
CC CHO CELLS, AND MEDIATED HSV ENTRY INTO ACTIVATED HUMAN T CELLS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABLE).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
CC IN LUNG, SPLEEN, AND THYMUS.
CC -1- SIMILARITY: CONTAINS 1 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC
CC EMBL; U70321; AAB58354.1; -
CC EMBL; U81232; AAD00505.1; -
CC EMBL; AF153978; AAF75588.1; -
CC HSSP; P25942; 1CDF.
CC MIM; 602746; -
```

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DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS00652; TNFR_NGFR_2; 2.
DR Receptor: Transmembrane; Glycoprotein; Repeat; Signal.
KW SIGNAL 1 38
FT CHAIN 39 283
FT DOMAIN 39 202
FT TRANSMEM 203 223
FT DOMAIN 224 283
FT DOMAIN 224 162
FT REPEAT 42 75
FT REPEAT 78 119
FT REPEAT 121 162
FT DISULFID 42 53
FT DISULFID 54 67
FT DISULFID 57 75
FT DISULFID 78 93
FT DISULFID 96 111
FT DISULFID 99 119
FT DISULFID 121 127
FT DISULFID 138 162
FT CARBOHYD 110 110
FT CARBOHYD 173 173
FT CONFLICT 17 17
FT CONFLICT K -> R (IN REF. 1).
SQ SEQUENCE 283 AA; 30392 MW; 46CE13C2C70242C1 CRC64;

Query Match 15.1%; Score 246; DB 1; Length 283;
Best Local Similarity 35.4%; Pred. No. 1.7e-12;
Matches 69; Conservative 16; Mismatches 88; Indels 22; Gaps 8;

QY 7 PGLSLCLVLALPAL---LPVPAVRGVAETPTYPWRDAETGERLVCAQCPGTFVORPCR 63
Db 16 PTDVLRLVLTFLGAPCYAPALPSCKE-DEYP-----VGSE-CCPKCSGPGYRVKEACG 68

QY 64 RSPTTCGCPPPHYTFQWNYLER---CRYCNVLCGEREEERACHATHNRACRRTGFF 120
Db 69 ELTGTVCEPCPGCTYIAHLNGLSKLCQCMCPAMGLR--ASRNCSTENAVCGCSFGHF 126

QY 121 A-----HAGFLEHASCPPGAGVIAPGTPSQNTQCPGPTFSASSSSSEOCQPHRNC 174
Db 127 CIVQDGDHCAACRAYATSSPGQVRQKGTESQDTLCQNCPPGTFPS-PNGTLEECQHQTKC 185

QY 175 TALGLALNVPGSSSH 189
Db 186 SWLVTKAGAGTSSSH 200

RESULT 7
VT2_SFVKA
ID VT2_SFVKA STANDARD; PRT; 325 AA.
AC P25943;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Shope fibroma virus (strain Kasza) (SFV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=10272;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=873221103; PubMed=2820128;
RA Upton C., Delange A.M., McFadden G.;
RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
RL telomeric region of the Shope fibroma virus genome.";
RN Virology 160:20-30(1987).
RN [2]
```

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RP FUNCTION.
RX MEDLINE=91207415; PubMed=1850261;
RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
RA McFadden G., Goodwin R.G.;
RT "T2 open reading frame from the Shope fibroma virus encodes a soluble
RT form of the TNF receptor.";
RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC
CC EMBL: M17433; -; NOT_ANNOTATED_CDS.
CC DR EMBL: A23727; CAA01687.1; -.
CC DR PIR: B43692; B43692.
CC DR HSSP: PI9438; ITNR.
CC DR InterPro: IPR001368; TNFR_c6.
CC DR Pfam: PF00020; TNFR_c6; 2.
CC DR ProDom: PD000771; TNFR_c6; 1.
CC DR SMART: SM00208; TNFR; 3.
CC DR PROSITE: PS00652; TNFR_NGFR_1; 2.
CC DR PROSITE: PS00652; TNFR_NGFR_2; 1.
CC DR Receptor; Glycoprotein; Repeat; Signal.
KW SIGNAL 1 16
FT CHAIN 17 325
FT DOMAIN 27 186
FT REPEAT 27 62
FT REPEAT 63 104
FT REPEAT 105 147
FT REPEAT 148 186
FT CARBOHYD 105 105
FT CARBOHYD 181 181
FT CARBOHYD 205 205
FT CARBOHYD 238 238
FT CARBOHYD 325 AA; 35132 MW; 81053039198A71E CRC64;
SQ SEQUENCE 325 AA; 35132 MW; 81053039198A71E CRC64;

Query Match 14.5%; Score 236.5; DB 1; Length 325;
Best Local Similarity 29.9%; Pred. No. 1.1e-11;
Matches 58; Conservative 25; Mismatches 94; Indels 17; Gaps 4;

QY 11 LLCLVLALPALPVPVAVRGVAETPTYPWRDAETGERLVCAQCPGTFVORPCRDSPTTC 70
Db 8 LVCVVYVYGDVFPYSSNQKCGGHDY-----EKDGLCCASCHPGFYASRLCGPGSNVTC 61

QY 71 GPCPPHYTFQWNYLERCRYCNVLCGEREEERACHATHNRACRRTGFFA-----HAG 124
Db 62 SPCEDTGTFSTASTNHAPACVSCRGPCGTHLSEQPCDTHDRVCNCSGTGNTCLLKQNGCR 121

QY 125 FCLEHASCPPGAGVIAPGTPSQNTQCPGPTFSASSSSSEOCQPHRNCATLGLALNVP 184
Db 122 ICAPQTKCPAGYGV-SGHTFRAGDTLCEKCPHYSDLSLPTERCSTSFNIVSGFNL--- 177

QY 185 GSSSHDTLCTSCGTG 198
Db 178 -YPVNETSCTTTAG 190

RESULT 8
OX40_HUMAN
ID OX40_HUMAN STANDARD; PRT; 277 AA.
AC P43489; Q13663;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
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Db 60 QNTVCRPCGPGFYNDVVSSKPKCTCNLRSRG--SERKQLCTATQDTVCRCRAG----- 112
Qy 124 GFCLHEASCPGAGVIAPGTPSQNTQCQPPGTFSSASSSSSEOCQPHRNCITGLGALNV 183
Db 113 --TQPLDSYKFG-----VDCAPCPGPHF--SPGDNQACKPWTNCTLAGKHTLQ 156
Qy 184 PGSSSHDTLCTS---CTGFPPLSTRVPGAECECAVIDEFAFQDISIKRLQLLQALEAPE 240
Db 157 PASNSSDAICEDRDPPATQPOGTGPPARPI-----TVQPTPE 193
Qy 241 GW-----GPTPR-----AGRAALQKLRRRLTELLGADGALLVRLLOALRVARWP 286
Db 194 AWPRTSOGSPSTRVEVPGGRAVAAILGLVLGLLGPL--AILLALYLLRRDQRLP 247

RESULT 9
VT2_MYXVL
ID VT2_MYXVL STANDARD; PRT; 326 AA.
AC P29825;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OC NCBI_TaxID=31530;
RN [1]
RX MEDLINE=91335768; PubMed=1651597;
RA Upton C., Macen J.L., Schreiber M., McFadden G.;
RT "Myxoma virus expresses a secreted protein with homology to the tumor
RT necrosis factor receptor gene family that contributes to viral
RT virulence";
RL Virology 184:370-382(1991).
CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC -----
CC EMBL; M95181; AAA46632.1; -.
CC EMBL; A23729; CAA01688.1; -.
CC PIR; A40566; GQV2ML.
CC HSP; P19438; ITNR.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 2.
CC ProDom; PD000771; TNFR_c6; 1.
CC SMART; SM00208; TNFR; 3.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 326
FT DOMAIN 27 186
FT REPEAT 27 62
FT REPEAT 63 104
FT REPEAT 105 147
FT REPEAT 148 186
FT CARBOHYD 66 66
FT CARBOHYD 181 181
FT CARBOHYD 205 205
FT CARBOHYD 238 238
FT SEQUENCE 326 AA; 35208 MW; ABBF027B947292FF CRC64;
FT TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT 4 X TNFR-CYS.
FT TNFR-CYS 1.
FT TNFR-CYS 2.
FT TNFR-CYS 3.
FT TNFR-CYS 4.
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT ABBF027B947292FF CRC64;

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ET TRAN





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Query Match      12.4%; Score 202; DB 1; Length 269;
Best Local Similarity 28.5%; Freq. No. 4.4e-09;
Matches 67; Conservative 20; Mismatches 122; Indels 26; Gaps 7;

QY 47 LVCAQCPGGTFVQPCRRDSPTTCGCPPHRYTQFWN---YLCRCRYCNVLCGEREEA- 102
      ||| |||
Db 36 LCDCLPQPGKGLNDCTEVSKTCQSGKGGEFTSTWNREKYCHEHRYCNFNLGRIOSEG 95
      ||| |||

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Search completed: May 10, 2002, 10:59:24  
Job time: 333 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 10, 2002, 10:52:31 ; Search time 24.1 Seconds  
(without alignments)  
948.231 Million cell updates/sec

Title: US-09-280-567-2  
Perfect score: 1634  
Sequence: 1 MRALGGPGLSLCLVLALPA.....RVAMPGLRSVRERFLPVH 300  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	351.5	21.5	461	1 A35356	tumor necrosis fac
2	333.5	20.4	459	2 I48854	gene murine tumour
3	332.5	20.3	474	2 B38634	tumor necrosis fac
4	315	19.3	435	2 I54182	tumor necrosis fac
5	262.5	16.1	349	2 D72175	G2R protein - vari
6	262.5	16.1	349	2 D36858	gene G4R protein -
7	262	16.0	348	2 T28623	hypothetical prote
8	236.5	14.5	325	2 B43692	T2 protein - rabbi
9	226	13.8	277	2 I37552	OX40 homolog - hum
10	215	13.2	326	1 G0VZML	T2 protein - myxom
11	214	13.1	271	2 S12783	OX40 antigen precu
12	211	12.9	277	2 A06071	B-cell activation
13	203	12.4	305	2 A46476	B cell-associated
14	198.5	12.1	272	2 I48700	gene ox40 protein
15	186.5	11.4	595	2 A42086	CD30 antigen precu
16	185	11.3	256	2 B32393	T-cell antigen 4-1
17	176	10.8	416	1 JN0006	nerve growth facto
18	175.5	10.7	427	1 G0HUN	nerve growth facto
19	174	10.6	255	2 I38426	lymphocyte activat
20	170	10.4	425	1 A26431	nerve growth facto
21	159.5	9.8	260	1 A46517	CD27 antigen precu
22	155.5	9.5	327	2 A46484	apoptosis-mediati
23	148.5	9.1	1574	2 T13954	MEG6 protein - ra
24	148	9.1	250	1 A49053	CD27 antigen precu
25	147.5	9.0	5376	2 T42215	zonadhesin - mouse
26	145	8.9	335	2 A40036	apoptosis-mediati
27	144	8.8	324	2 JC2395	Fas antigen precu
28	143.5	8.8	1299	2 T43251	furin (EC 3.4.21.7
29	143	8.8	1620	2 T27283	hypothetical prote

30 140 8.6 314 2 I37383 FAS soluble protei  
31 137.5 8.4 454 1 GQMST1 tumor necrosis fac  
32 135 8.3 2321 2 S78549 notch3 protein - h  
33 133 8.1 493 2 JC5486 membrane glycoprot  
34 129.5 7.9 1548 2 S34583 serine proteinase  
35 128.5 7.9 3635 2 T10053 laminin alpha 5 ch  
36 127 7.8 1192 2 S69000 laminin gamma 2 ch  
37 125.5 7.7 461 1 GQRTT1 tumor necrosis fac  
38 125.5 7.7 1255 1 A24571 protein-tyrosine k  
39 124.5 7.6 1713 2 A55347 adhesive ligand ep  
40 124.5 7.6 3106 1 S53868 laminin alpha-2 ch  
41 123.5 7.6 455 1 GQHUT1 tumor necrosis fac  
42 122.5 7.5 2824 2 T22759 hypothetical prote  
43 120 7.3 1609 1 MHUB2 laminin gamma-1 ch  
44 120 7.3 2318 2 S45306 notch 3 protein -  
45 119.5 7.3 461 2 JC4302 tumor necrosis fac

ALIGNMENTS

RESULT 1  
A35356  
tumor necrosis factor receptor 2 precursor [validated] - human  
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000  
C:Accession: A35356; A36475; A36007; A23666; B35010; I38094  
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dover, Science 248, 1019-1023, 1990  
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular a  
A:Reference number: A35356; MUID:90260639  
A:Accession: A35356  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <SMI>  
A:Cross-references: GB:M32315; NID:q189185; PIDN:AAA59929.1; PID:q189186  
R:Kohnho, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc  
A:Reference number: A36475; MUID:91045991  
A:Accession: A36475  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195, 'R', 197-461 <KOH>  
A:Cross-references: GB:M55994; GB:M38549; NID:q339757; PIDN:AAA36755.1; PID:q339758  
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990  
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular  
A:Reference number: A48416; MUID:91370690  
A:Accession: A48416  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-461 <DEM>  
A:Cross-references: GB:S63368; NID:q235648; PIDN:AAB19824.1; PID:q235649  
A:Note: sequence extracted from NCBI backbone (NCBI:63368, NCBI:63371)  
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons  
A:Reference number: A36007; MUID:90349572  
A:Accession: A36007  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>  
A:Cross-references: GB:M35857; NID:q339751; PIDN:AAA63262.1; PID:q339752  
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990  
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor  
A:Reference number: A23666; MUID:91056048  
A:Accession: A23666  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>

R:Engelmann, H.; Novick, D.; Wallach, D.  
 J. Biol. Chem. 265, 1531-1536, 1990  
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
 A:Reference number: A35010; MUID:90110215  
 A:Accession: B35010  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 27-31 <ENG>  
 R:Kuhnert, P.; Kemper, O.; Wallach, D.  
 Gene 150, 381-386, 1994  
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of  
 A:Reference number: 138094; MUID:95121934  
 A:Accession: 138094  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-37 <RES>  
 A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701  
 C:Genetics: GDB:TNFR2  
 A:Gene: GDB:TNFR2  
 A:Cross-references: GDB:125914; OMIM:191191  
 A:Map position: lp36.2-lp36.2  
 A:Introns: 26/3  
 A>Note: the list of introns is incomplete  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>  
 F:40-76/Domain: NGF receptor repeat homology <NG1>  
 F:78-119/Domain: NGF receptor repeat homology <NG2>  
 F:120-162/Domain: NGF receptor repeat homology <NG3>  
 F:164-201/Domain: NGF receptor repeat homology <NG4>  
 F:262-279/Domain: transmembrane #status predicted <TMN>  
 F:280-461/Domain: intracellular #status predicted <INT>  
 F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.5%; Score 351.5; DB 1; Length 461;  
 Best Local Similarity 29.8%; Pred. No. 4.5e-19;  
 Matches 96; Conservative 43; Mismatches 122; Indels 61; Gaps 12;

QY 8 GLSLCLVLAALLPVPVAVRGVATPTVPRDAETGE-----RLVCAQCPPG 55  
 DB 13 GLELWAAHALPA-----QVATTPAP----EPGTCRLREYDQTAQCCSKSPG 60  
 QY 56 FTVPQPCRRDSTTCGPPRRHYTFWNYLRCRYCNVLCGRERARACHATHNRACR 115  
 DB 61 QHAKVCTKSTVDCSDSTYTTLWNVPCLSGCRSDQVETQACTREQNRICTC 120  
 QY 116 RTGFFAHAG-----FCLHASCPCGAGVIAPTGTPSNTQCPGPTFSASSSSEQCQ 169  
 DB 121 RFGWYCALSKOEGRLCAPLRKCRPGFGVAREGTETSDVVKPCAPGTFSTNTSDICR 180  
 QY 170 PHRNCTALGLALNVPGSSHDPLCTSCGTFPLSTRVPGAECERAAVIDFVAFQDISIKRL 229  
 DB 181 PHQICNVVA----IFGNASMDAVCTSTS--PTRSNAPGAVHLPPQV-----STRSQHT 227  
 QY 230 QRLQALFAPE-----GWGPTTPRA----GRAALQKLRRLRTELLGADGALLVRLQLAL 280  
 DB 228 QPTPEPTAPSTPSFLPLMGSPSPAGSGTGDFALPGLVIGVTAL-----GLLIIGVNCV 282  
 QY 281 ----RVARMP-GLERSVRERFLP 298  
 DB 283 IMTVQKKRKLCLQREAKVPHLP 304

RESULT 2  
 148854  
 gene murine tumor necrosis factor receptor 2 protein - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999  
 R:Accession: 148854  
 R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.  
 Mamm. Genome 5, 726-727, 1994

A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
 A:Reference number: I48854; MUID:95178848  
 A:Accession: I48854  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-459 <RES>  
 A:Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 20.4%; Score 333.5; DB 2; Length 459;  
 Best Local Similarity 29.7%; Pred. No. 1e-17;  
 Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps 9;

QY 46 RLVCACCPGTVQPCRRDSTTCGPPRRHYTFWNYLRCRYCNVLCGRERARAC 105  
 DB 37 QMCCARCPGQVKKFKNKTSDTVACDCEASMYTQVNNQFRTCLSCSSCSTDQVETAC 96  
 QY 106 HATHNRACRCRTGFF----AHAGF----CLEHASCPCGAGVIAPTGTPSNTQCPGPTGTF 158  
 DB 97 TKQONRVCAACEAGRYCALXTHSGSCRCQMRSLKCGFGVASSRAPNGNVLCACAPGTF 156  
 QY 159 SASSSSSEQCQPHRNTALGLALNVPGSSHDPLCT----SCGTFPLSTRVPGAECERA 214  
 DB 157 SDTTSSTDVCRPHRCSILA----IPGNASTDAVCAPESPTLSAIPRTLIVVSQPEPTRSQ 212  
 QY 215 VIDFVAFODISIKRLQRLQALEAPGSGWGP-----RAGRAALQKLRRLRTELLGADQ 269  
 DB 213 PLD-----QEPGSPQTPSILTSL-----GSTPIEOSTKGISLPIGLIVGVTSL----- 257  
 QY 270 GALLVRLQAL----RVARMPGLERSVRERFLP 298  
 DB 258 GLLMGLVNCFLVQKKPKSCLOQDAKVPHPV 290

RESULT 3  
 B38634  
 tumor necrosis factor receptor type 2 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
 R:Accession: B38634; A40254; S54816  
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,  
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto  
 A:Reference number: A38634; MUID:91187885  
 A:Accession: B38634  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <LEW>  
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
 R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J  
 Mol. Cell. Biol. 11, 3020-3026, 1991  
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f  
 A:Reference number: A40254; MUID:91246168  
 A:Accession: A40254  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <GOO>  
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
 R:Kisssonergis, M.; Fellows, R.; Feldmann, M.; Chernajovsky, Y.  
 submitted to the EMBL Data Library, May 1995  
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor  
 A:Reference number: S54816  
 A:Accession: S54816  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-22 <KIS>  
 C:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA0618.1; PID:g809044  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 C:Keywords: cytokine receptor; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
 F:40-77/Domain: NGF receptor repeat homology <NGI>  
 F:79-120/Domain: NGF receptor repeat homology <NG2>

F:166-203/Domain: NGF receptor repeat homology <NG4>

```
Query Match          20.3%; Score 332.5; DB 2; Length 474;
Best Local Similarity 29.7%; Pred. No. 1.2e-17;
Matches 81; Conservative 44; Mismatches 109; Indels 39; Gaps 9;

QY 46 RLVCACQPGCTFVQPCRRDSTTCGCPPRHYTQFWNYLERCRYCNVLCGEREEARAC 105
DB 52 QMCCAKCPGQVQHFCKNTSDTVACDASMYTQVMNQFRTCLSSSCTTDOVEIRAC 111
QY 106 HATHNRCRCRTGFF---AHAGE---CLEHASCPPGAGVIAPGTPSQNTQCPQPGTF 158
DB 112 TKQNRVACAGRCVYALKTHSGRCQWRLSKCGPFGVSSRAPNGNVLCACAPGTF 171
QY 159 SASSSSQCOQPHRNTALGLALNVPGSSSHDTLCT---SCTGFPLSTRVPGAECE 214
DB 172 SDTTSSTDCVRPHRCSILA---IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQ 227
QY 215 VIDFVAFODISIKRLQRLQALEAPEGWGTP-----RAGRAALQKLRRRLTELLGAQD 269
DB 228 PLD---QEPGPSQTPSILTSL-----GSTPIEQSTKGISLPIGLIVGVTSL----- 272
QY 270 GALLVRLQAL----RVARMPLGLSVRERFLP 298
DB 273 GLLMLGLVNCIILVQRKKRPSCLQORDAKVPHVP 305

RESULT 4
154182
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: I54182
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A:Reference number: I54182; MUID:93352381
A:Accession: I54182
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
```

```
Query Match          19.3%; Score 315; DB 2; Length 435;
Best Local Similarity 31.8%; Pred. No. 2.3e-16;
Matches 89; Conservative 29; Mismatches 120; Indels 42; Gaps 12;

QY 3 ALEGPGLSLLCLVLPALLPVPVGVVAETPTY-----PWRDA-----ETGERLYCAQC 52
DB 6 ATSAFGLANGPLVLGFLGLAASQPAV---PPYASENOTCRDQEKYEYEPQHRICCSRC 62
QY 53 PPGTFVQPCRRDSTTCGCPPRHYTQFWNYL---ERCRCYNVLCGEREEARACHATH 109
DB 63 PPGTVYSAKCSRIRDTVCATCAENSYNHWNVLTICQLCRCPDPVNG--LEETAPCTSKR 120
QY 110 NRACRCRTGFFAHAGFCLE--H-----ASCPPGA-GVIAPGTPSQNTQCPQPGTFSASS 162
DB 121 KTCRCQCPGMFC-AAWALACTHCELLSDCPGTEAELKDEVGKGNHNCVPCKAGHFQNTS 179
QY 163 SSSECOQPHRNTALGLALNVPGSSSHDTLCTSGCTGFPLSTRVPGAECECAVIDFVAFQ 222
DB 180 SPSCQCPHTRCENQGLVBAAPGTAQSDTCKNPLE-PLPPMSGTMMLAVLLPLAFL 238
QY 223 DIS-----IKRLQRLQALEAPEGWGTPPRAG 249
DB 239 LLATVSCITKWSHPSLCRLKLSILK--RRPQEGGNPVAG 276
```

```
RESULT 5
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C>Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C:Accession: D72175
R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lo
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola mi
A:Reference number: A72150
A:Accession: D72175
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <SHC>
A:Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: G2R
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match          16.1%; Score 262.5; DB 2; Length 349;
Best Local Similarity 30.0%; Pred. No. 1.6e-12;
Matches 62; Conservative 29; Mismatches 103; Indels 13; Gaps 3;

QY 9 LSLCLVLVLPALLPVPVGVVAETPTYPMWDAETGERLYCAQCQPGCTFYQPCRRDSPT 68
DB 10 LFLSCIIINGRDAAPYTPPNCKCKDTEY-----KRHLCLCLSCPPGCTYASRLCDSKTNT 63
QY 69 TCGPCPRHYTQFWNYLERCRYCNVLCGEREEARACHATHNRCRCRTGFF-----AH 122
DB 64 QCTPGSGTFTSRNNHLPACLSCGRCNSQVTRSCNTTHNRICEGSPGYCILLKGSSG 123
QY 123 AGCFLHASCPCPGAGVIAPGTPSQNTQCPQPGTFSASSSSSECOQPHRNTALGLALN 182
DB 124 CKACVSQTKGIGYGV-SGHTSVGDVICSPCGFGTYSTVTSSTDKCEPVNPNFTNYIDVE 182
QY 183 VPGSSSHDTLCTSGCTGFPLSTRVPGAE 209
DB 183 ITLPVPNDTSCRTTITGLSEILTSE 209

RESULT 6
D36858
gene G4R protein - variola virus
N:Alternate names: B28R protein (COP)
C:Species: variola virus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C:Accession: D36858; S46888; S32385; S35987
R:Blinov, V.M.
A:Reference number: A36859
A:Reference number: A36859
A:Accession: D36858
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <BLI>
A:Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A:Experimental source: strain India-1967, ssp. major, isolate Ind3
R:Kolykhalov, A.A.; Blinov, V.M.; Gutorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; F
submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H
A:Reference number: S46868
A:Accession: S46888
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <KOL>
A:Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A:Experimental source: strain India-1967, isolate Ind3
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protect
```

A:Reference number: S32385; MUID:93202281

A:Accession: S32385

A:Molecule type: DNA

A:Residues: 31-168 <SHC>

A:Cross-references: EMBL:X69198

A:Experimental source: strain India-1967, ssp. major

A:Genetics: G4R

C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

F:32-66/Domain: NGF receptor repeat homology <NGF>

F:68-109/Domain: NGF receptor repeat homology <NG2>

F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 16.1%; Score 262.5; DB 2; Length 349;  
Best Local Similarity 30.0%; Pred. No. 1.6e-12;  
Matches 62; Conservative 29; Mismatches 103; Indels 13; Gaps 3;

QY 9 LSLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPTGTFVQRPCTDPT 68

DB 10 LFLSCLIIINGRDAAPYTPNGKCKDTEY-----KRNLCCLSCPPGTYASRLCDSKTNT 63

QY 69 TCGPCPPRHYYTFQWNYLERCRVNCVLCGEREEARACHATHNRACRGTGFF-----AH 122

DB 64 QCTPCGSGTFTSRNHLPACLSCNGRCNSNQVETRSCNTTHNRICBCSPGYCYLLKGSSG 123

QY 123 AGFCLHASCPCPGAGVIAPGTPSQNTQCPQPPGTFSSASSSSSQCPHRCNTALGLALN 182

DB 124 CRACVSQTKCGIGYV-SGHTSVGDVICSFGCGFYSHTVSSADKCEPVNNTFNVDYE 182

QY 183 VFGSSSHDTLCTSCGTFPLSTRVPGAE 209

DB 183 ITILPVNDTSCRTTTTGLSEILTSE 209

RESULT 7

T28623

hypothetical protein G2R - variola major virus

C:Species: variola major virus

C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000

C:Accession: T28623

R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin

Nature 366, 748-751, 1993

A:Title: Potential virulence determinants in terminal regions of variola smallpox virus

A:Reference number: 220488; MUID:94088747

A:Accession: T28623

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-348 <MAS>

A:Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102

A:Experimental source: strain Bangladesh 1975

C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 16.0%; Score 262; DB 2; Length 348;  
Best Local Similarity 30.8%; Pred. No. 1.7e-12;  
Matches 64; Conservative 28; Mismatches 100; Indels 16; Gaps 4;

QY 9 LSLCLVLALPALLPVPVAVRGVAETPTYPWRDAE-TGERLVCAQCPTGTFVQRPCTDPT 67

DB 10 LFLSCLIIINGRDAAPYTP-----PNGKCKDTEYKRNLCCLSCPPGTYASRLCDSKTNT 61

QY 68 TTCGCPPPRHYYTFQWNYLERCRVNCVLCGEREEARACHATHNRACRGTGFF-----A 121

DB 62 TOCTPCGSGTFTSRNHLPACLSCNGRCNSNQVETRSCNTTHNRICBCSPGYCYLLKGSS 121

QY 122 HAGFCLHASCPCPGAGVIAPGTPSQNTQCPQPPGTFSSASSSSSQCPHRCNTALGLAL 181

DB 122 GCKACVSQTKCGIGYV-SGHTSVGDVICSFGCGFYSHTVSSADKCEPVNNTFNVDY 180

QY 182 NVPGSSSHDTLCTSCGTFPLSTRVPGAE 209

DB 181 EITLIPVNDTSCRTTTTGLSEILTSE 208

RESULT 8

B43692

T2 protein - rabbit fibroma virus

C:Species: rabbit fibroma virus, Shope fibroma virus

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C:Accession: B43692

R:Upton, C.; Delange, A.M.; McFadden, G.

Virology 160, 20-30, 1987

A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomer

A:Reference number: A43692; MUID:87321103

A:Accession: B43692

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-325 <UPT>

A:Cross-references: GB:M17433

C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

F:64-105/Domain: NGF receptor repeat homology <NG2>

F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 14.5%; Score 236.5; DB 2; Length 325;  
Best Local Similarity 29.9%; Pred. No. 1.3e-10;  
Matches 58; Conservative 25; Mismatches 94; Indels 17; Gaps 4;

QY 11 LLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPTGTFVQRPCTDPTTC 70

DB 8 LCVVVVYGVDDVPYSSNOCKGGHDY-----EKDGLCCASCHPGFYASRLCGPGSNTVC 61

QY 71 GPCPPPHYYTFQWNYLERCRVNCVLCGEREEARACHATHNRACRGTGFFA-----HAG 134

DB 62 SPEDCGTFTASTNHAPACVSCRGPCCTGHLSEQPCDRTDHRVNCSTGNYCLLKQNGCR 121

QY 125 FCLHASCPCPGAGVIAPGTPSQNTQCPQPPGTFSSASSSSSQCPHRCNTALGLALNVP 184

DB 122 ICAPQTKCPAGYGV-SGHTRAGDTLCEKCPHTYSDLSPTERCSTGTFNYSVGFNL--- 177

QY 185 GSSSHDTLCTSCGT 198

DB 178 -YPVNETSCTTTAG 190

RESULT 9

I37552

OX40 homolog - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000

C:Accession: I37552

R:Lataza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo

Eur. J. Immunol. 24, 677-683, 1994

A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment

A:Reference number: I37552; MUID:94170844

A:Accession: I37552

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-277 <RES>

A:Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958

C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 13.8%; Score 226; DB 2; Length 277;  
Best Local Similarity 27.0%; Pred. No. 6.6e-10;  
Matches 80; Conservative 25; Mismatches 117; Indels 74; Gaps 12;

QY 6 GGLSLLCLLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPTGTFVQRPCTDPT 65

DB 11 GFCAALLLGLSLSTVTGLHCY-----GDTYPSNDR-----CCHCEPFGNGMVSRCSRS 59

QY 66 SPTTCGCPPHYYTFQWNYLERCRVNCVLCGEREEARACHATHNRACRGTGFFA 123

DB 60 QNTVCRPCGPGFYNDVSSKPKCTWCNLRSG--SERKQLCTATQDTVCRCRAG----- 112



QY 124 GFCLEHASCPPGAGVIAPGTPSONTOCOPCPPTFSASSSSSQOPHRNCTALGLALNV 183  
Db 113 --TQPLDSTKPG-----VDCACPPGGHF--SPGDNOACKPWTNCTLAGKHTLQ 156  
QY 184 PGSSSHDTLCTS---CTGFPLSTRVPGABECERAVIDFAFQDISIKRLQLLQALEAPE 240  
Db 157 PASNSSDAICDRDPATQETQGGPARPI-----TWQPT 193  
QY 241 GW-----GTPPR-----AGRAALQLKRLRRLTELLGAQDQCALLVRLQLARVARMP 286  
Db 194 AWPRTSQGSPSTRVPPGGRVAAAILGLVLGLLGLPL--AAILLALLRRDQRLP 247  
RESULT 10  
GQVZML  
T2 protein - myxoma virus (strain Lausanne)  
C:Species: myxoma virus  
C:Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 18-Jun-1999  
C:Accession: A40566  
R:Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.  
Virology 184, 370-382, 1991  
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis  
A:Reference number: A40566; MUID:91335768  
A:Accession: A40566  
A:Molecule type: DNA  
A:Residues: 1-326 <UPT>  
A:Cross-references: GB:M95181; GB:M37976; NID:g3323309; PIDN:AAA46632.1; PID:g3323310  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
C:Keywords: glycoprotein  
F:64-105/Domain: NGF receptor repeat homology <NG2>  
F:106-147/Domain: NGF receptor repeat homology <NG3>  
F:66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.2%; Score 215; DB 1; Length 326;  
Best Local Similarity 29.3%; Pred. No. 5.1e-09;  
Matches 58; Conservative 22; Mismatches 96; Indels 22; Gaps 5;  
QY 12 LCILVLALPALL-----PVPARGVAVETPTYPWRDAETGERLVCAQCPPTGFVORPCRRDS 66  
Db 4 LTLALLAYACVYGGGAPYADRGKRGNDY-----EKDGLCTSPGSGYASRLCGPGS 57  
QY 67 PTCGCPPRHYTOFWNYLRCRYCNVLCGEREEARACHATHNRACRCRTGFFA----- 121  
Db 58 DIVCSCKNETFTASTNHAPACVSCRGRTGHLSEQSCKDTRDVCDSAGNYCILLKQ 117  
QY 122 -HAGFLEHASCPPGAGVIAPGTPSONTOCOPCPPTFSASSSSSQOPHRNCTALGLA 180  
Db 118 EGCRCAPKTKCPAGXGV-SGHRTRGDVLCTKCPRTYSDAVSSTETCTSSFNVISVEFN 176  
QY 181 LNVPGSSSHDTLCTSG 198  
Db 177 L-----YPVNDTCTTTAG 190  
RESULT 11  
S12783  
OX40 antigen precursor - rat  
N:Alternate names: nerve growth factor receptor homolog  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C:Accession: S12783; S08036  
R:Wallett, S.; Fossum, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990  
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte  
A:Reference number: S12783; MUID:90214614  
A:Accession: S12783  
A:Molecule type: mRNA  
A:Residues: 1-271 <MAT>  
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: growth factor receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-271/Product: OX40 antigen #status predicted <MAT>  
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 13.1%; Score 214; DB 2; Length 271;  
Best Local Similarity 30.1%; Pred. No. 5.1e-09;  
Matches 58; Conservative 23; Mismatches 64; Indels 48; Gaps 9;  
QY 10 SLCLVLALPALLPVPARGVAVETPTYPWRDAETGERLVCAQCPPTGFVORPCRRDSPTT 69  
Db 10 AFLLLGLSLGVTVKLNCVK-----DTYP-----SGHK-CCRECQPGHGMVSRCDHTRDTV 58  
QY 70 CGPCPPRHYTOFWNY--LERCRCYCNVLCGEREEARACHATHNRACRCRTGFFAHAGFCL 127  
Db 59 CHFCEPGFYNEAVNYDTCKQCTQCNRHS--SELKNCTPTEDTVCCOR----- 105  
QY 128 EHASCPPGAGVIAPGT-PSQNT-----QCPCPPPTGFSSASSSSSQOPHRNCTALGLA 180  
Db 106 -----PGTQPRDSSSHKLGVDVCPGPGHF--SPGSNOACKPWTNCTLSGKQ 150  
QY 181 LNVPGSSSHDTLCT 193  
Db 151 IRHPASNSLDTVC 163  
RESULT 12  
A60771  
B-cell activation protein CD40 precursor - human  
N:Alternate names: B-cell surface antigen Bp50  
C:Species: Homo sapiens (man)  
C:Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000  
C:Accession: S04460; A60771  
R:Stamenkovic, I.; Clark, E.A.; Seed, B.  
EMBO J. 8, 1403-1410, 1989  
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor  
A:Reference number: S04460; MUID:89356608  
A:Accession: S04460  
A:Molecule type: mRNA  
A:Residues: 1-277 <STA>  
A:Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851  
R:Brasch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.  
J. Immunol. 142, 562-567, 1989  
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-  
A:Reference number: A60771; MUID:89093941  
A:Accession: A60771  
A:Molecule type: protein  
A:Residues: 21-50 <BRA>  
A:Experimental source: Burkitt lymphoma cell line Raji  
C:Genetics:  
A:Gene: GDB:CD40  
A:Cross-references: GDB:215268; OMIM:109535  
A:Map position: 20q12-20q13.2  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>  
F:21-193/Domain: extracellular #status predicted <EXT>  
F:194-215/Domain: transmembrane #status predicted <TM>  
F:216-277/Domain: intracellular #status predicted <CYT>  
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.9%; Score 211; DB 2; Length 277;  
Best Local Similarity 30.5%; Pred. No. 8.8e-09;  
Matches 46; Conservative 21; Mismatches 76; Indels 8; Gaps 3;  
QY 49 CAOCPPGTFVQRCRRDSDPTTCGCPPRHYTOFWNYLRC-----RYCNVLCGEREEARAC 105  
Db 38 CSLCQPGQKLVSDCTETETECPLCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTS 97  
QY 106 HATHNRACRRTGFFAFA-----GFLCHHACPPGAGVIAPGTPSONTOCOPCPPTFSASS 162  
Db 98 ET--DTICTCEGWHTCTSEACESCVLHRSCTPGFGVKQIATGVSDTICEPCVPGFFSNVS 155



Db 10 LLFLGALRAFPQDRPEDTCHGNPSHY---DKAVRCCYRCPMGLFPTQOCQ-RPTDC 65  
Qy 71 -GPCPPRHYTOFWNYLERCRYCNVLCGERE-EARACHATHNRACRRTGFFAHAGF--- 125  
Db 66 RKOCEPDYLL---DEADRCTAC-VTCSRDDLVEKTPCAWNSRVCRCRPMFCSTSAVNS 121  
Qy 126 ---CLEHASCPPCAGVIAPGTPSONTCOCOPCPGTFESASSSSSEOCQ-----PHRNCT 175  
Db 122 CARCFHSHVCPAGMIVKFPGTAKNTVCEPASPGV-SPACASPENCKEPSSSGTIPQAKPT 180  
Qy 176 ALGLALNVFGSSSHDTL 192  
Db 181 PVS-----PATSSASTM 192

Search completed: May 10, 2002, 10:54:20  
Job time: 109 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 10:52:31 ; Search time 22.98 Seconds  
(without alignments)  
293.777 Million cell updates/sec

Title: US-09-280-567-2  
Perfect score: 1634  
Sequence: 1 MRALGPGLSLLCLVLALPA.....RVARMPGLRSVRERFLPVH 300

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A-COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B-COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A-COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B-COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS-COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1634	100.0	300	2	US-08-794-796-2
2	1619.5	99.1	299	4	US-09-286-529-17
3	1177	72.0	211	4	US-09-286-529-20
4	841	51.5	153	4	US-09-286-529-2
5	444	27.2	401	3	US-08-974-022-6
6	444	27.2	401	4	US-09-042-785A-12
7	444	27.2	401	4	US-08-795-445A-6
8	444	27.2	401	4	US-08-795-447A-6
9	444	27.2	401	4	US-08-974-186-6
10	444	27.2	401	4	US-08-795-446B-6
11	444	27.2	401	4	US-09-153-927-1
12	425.5	26.0	401	3	US-08-974-022-2
13	425.5	26.0	401	4	US-08-795-445A-2
14	425.5	26.0	401	4	US-08-795-447A-2
15	425.5	26.0	401	4	US-08-974-186-2
16	425.5	26.0	401	4	US-08-795-446B-2
17	424.5	26.0	401	3	US-08-974-022-4
18	424.5	26.0	401	4	US-09-042-785A-13
19	424.5	26.0	401	4	US-08-795-445A-4
20	424.5	26.0	401	4	US-08-795-447A-4
21	424.5	26.0	401	4	US-08-974-186-4
22	424.5	26.0	401	4	US-08-795-446B-4
23	353.5	21.6	461	4	US-09-042-785A-7
24	353.5	21.5	461	4	US-09-006-353A-4
25	351.5	21.5	461	1	US-08-385-229-2
26	351.5	21.5	461	2	US-08-650-000-2
27	351.5	21.5	461	4	US-08-477-347-3

28	351.5	21.5	461	4	US-08-476-862-2	Sequence 2, Appl1
29	351.5	21.5	461	6	5395760-2	Patent No. 5395760
30	346	21.2	227	3	US-08-974-022-48	Sequence 48, Appl1
31	346	21.2	227	4	US-08-795-445A-48	Sequence 48, Appl1
32	346	21.2	227	4	US-08-795-447A-48	Sequence 48, Appl1
33	346	21.2	227	4	US-08-974-186-48	Sequence 48, Appl1
34	346	21.2	227	4	US-08-795-446B-48	Sequence 48, Appl1
35	344	21.1	486	1	US-08-243-010-1	Sequence 1, Appl1
36	344	21.1	518	1	US-08-385-229-4	Sequence 4, Appl1
37	335	20.5	235	4	US-09-326-394-4	Sequence 4, Appl1
38	332.5	20.3	474	2	US-08-650-000-4	Sequence 8, Appl1
39	332.5	20.3	474	4	US-09-042-785A-8	Sequence 5, Appl1
40	332.5	20.3	474	6	5395760-4	Patent No. 5395760
41	318	19.5	163	2	US-08-219-237B-5	Sequence 5, Appl1
42	318	19.5	163	4	US-08-477-347-13	Sequence 13, Appl1
43	318	19.5	163	4	US-08-476-862-4	Sequence 4, Appl1
44	318	19.5	163	4	US-08-468-560C-5	Sequence 5, Appl1
45	316	19.3	164	2	US-08-232-087A-9	Sequence 9, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-794-796-2  
; Sequence 2, Application US/08794796  
; Patent No. 5885800  
; GENERAL INFORMATION:  
; APPLICANT: Emery, John  
; APPLICANT: Tan, KB  
; APPLICANT: Truneh, Alem  
; APPLICANT: Young, Peter  
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,  
; TITLE OF INVENTION: TR4  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/794,796  
; FILING DATE: 04-FEB-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Han, William T  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: GH50000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-4026  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 300 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-794-796-2

Query Match 100.0%; Score 1634; DB 2; Length 300;

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Best Local Similarity 100.0%; Pred. No. 1.9e-127;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALEGPGLSLLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLYCAQCPPGTFFVQR 60
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Db 1 MRALEGPGLSLLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLYCAQCPPGTFFVQR 60
    |||||||

Qy 61 PCRRDSPITTCGPPRHYTOFWNYLRCRYCNVLCGEREEERACHATHNRACRCRTGFF 120
    |||||||
Db 61 PCRRDSPITTCGPPRHYTOFWNYLRCRYCNVLCGEREEERACHATHNRACRCRTGFF 120
    |||||||

Qy 121 AHAGFCLEHASCPCPGAGVIAPGTPSQNTQCPCPPGTFSASSSSEQCQPHRNCTALGLA 180
    |||||||
Db 121 AHAGFCLEHASCPCPGAGVIAPGTPSQNTQCPCPPGTFSASSSSEQCQPHRNCTALGLA 180
    |||||||

Qy 181 LNVPGSSSHDITLCTSGTGFPLSTRVPGAECEERAVIDFVAFODISIKRLQLQALEAPE 240
    |||||||
Db 181 LNVPGSSSHDITLCTSGTGFPLSTRVPGAECEERAVIDFVAFODISIKRLQLQALEAPE 240
    |||||||

Qy 241 GWGPTPRAGRAALQLKRRRLTELLGAODGALLVRLQALVARMPGLSRRERFLPVH 300
    |||||||
Db 241 GWGPTPRAGRAALQLKRRRLTELLGAODGALLVRLQALVARMPGLSRRERFLPVH 300
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RESULT 2
US-09-286-529-17
; Sequence 17, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286.529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-17
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Query Match 99.1%; Score 1619.5; DB 4; Length 299;
Best Local Similarity 99.7%; Pred. No. 3e-126;
Matches 299; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MRALEGPGLSLLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLYCAQCPPGTFFVQR 60
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Db 1 MRALEGPGLSLLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLYCAQCPPGTFFVQR 60
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Qy 61 PCRRDSPITTCGPPRHYTOFWNYLRCRYCNVLCGEREEERACHATHNRACRCRTGFF 120
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Db 61 PCRRDSPITTCGPPRHYTOFWNYLRCRYCNVLCGEREEERACHATHNRACRCRTGFF 120
    |||||||

Qy 121 AHAGFCLEHASCPCPGAGVIAPGTPSQNTQCPCPPGTFSASSSSEQCQPHRNCTALGLA 180
    |||||||
Db 121 AHAGFCLEHASCPCPGAGVIAPGTPSQNTQCPCPPGTFSASSSSEQCQPHRNCTALGLA 179
    |||||||

Qy 181 LNVPGSSSHDITLCTSGTGFPLSTRVPGAECEERAVIDFVAFODISIKRLQLQALEAPE 240
    |||||||
Db 180 LNVPGSSSHDITLCTSGTGFPLSTRVPGAECEERAVIDFVAFODISIKRLQLQALEAPE 239
    |||||||

Qy 241 GWGPTPRAGRAALQLKRRRLTELLGAODGALLVRLQALVARMPGLSRRERFLPVH 300
    |||||||
Db 240 GWGPTPRAGRAALQLKRRRLTELLGAODGALLVRLQALVARMPGLSRRERFLPVH 299
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RESULT 3
US-09-286-529-20
; Sequence 20, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
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; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286.529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-20

Query Match 72.0%; Score 1177; DB 4; Length 211;
Best Local Similarity 99.0%; Pred. No. 6.1e-90;
Matches 208; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRALEGPGLSLLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLYCAQCPPGTFFVQR 60
    |||||||
Db 1 MRALEGPGLSLLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLYCAQCPPGTFFVQR 60
    |||||||

Qy 61 PCRRDSPITTCGPPRHYTOFWNYLRCRYCNVLCGEREEERACHATHNRACRCRTGFF 120
    |||||||
Db 61 PCRRDSPITTCGPPRHYTOFWNYLRCRYCNVLCGEREEERACHATHNRACRCRTGFF 120
    |||||||

Qy 121 AHAGFCLEHASCPCPGAGVIAPGTPSQNTQCPCPPGTFSASSSSEQCQPHRNCTALGLA 180
    |||||||
Db 121 AHAGFCLEHASCPCPGAGVIAPGTPSQNTQCPCPPGTFSASSSSEQCQPHRNCTALGLA 180
    |||||||

Qy 181 LNVPGSSSHDITLCTSGTGFPLSTRVPGAE 210
    |||||||
Db 181 LNVPGSSSHDITLCTSGTGFPLSTRVPGEP 210
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RESULT 4
US-09-286-529-2
; Sequence 2, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286.529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 153
; TYPE: PRT
; ORGANISM: human
US-09-286-529-2
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Query Match 51.5%; Score 841; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.1e-62;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 LERCRCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCPGAGVIAPGTP 144
    |||||||
Db 1 LERCRCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCPGAGVIAPGTP 60
    |||||||

Qy 145 SONTQCPCPPGTFSASSSSEQCQPHRNCTALGLALNVPGSSSHDITLCTSGTGFPLSTR 204
    |||||||
Db 61 SONTQCPCPPGTFSASSSSEQCQPHRNCTALGLALNVPGSSSHDITLCTSGTGFPLSTR 120
    |||||||

Qy 205 VPGAEECERAVIDFVAFODISIKRLQLQALE 237
    |||||||
Db 121 VPGAEECERAVIDFVAFODISIKRLQLQALE 153
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RESULT 5
US-08-974-022-6
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; Sequence 6, Application US/08974022  
; Patent No. 6015938

## GENERAL INFORMATION:

; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,022  
; FILING DATE: 12-DEC-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 401 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-974-022-6

Query Match 27.2%; Score 444; DB 3; Length 401;

Best Local Similarity 39.6%; Pred. No. 3.6e-29;

Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LCLVLALPALLPVPAVRGVAET--PTYPRDAETGERLVCAQCPTGTFVQPCRRDST 68

Db 4 LCCAL---VFLDISIKWTQETFPKYLHYDEETSHQLLCKDCPPGTYLKQHCTAKWT 60

QY 69 TCGPCPPRHVTOFWNYLRCRYCNVLCGEREEARACHATHNRACRRTGFFAHAGFCLE 128

Db 61 VCAPCPDHYTDSWHTSDCLYCSPVKELQYVKQECNTRHNRVCECKEGRYLEIEFCLK 120

QY 129 HASCPPGAGVIAPGTPSQNTQCPQPPGTFSSSSSEQCPHRNCTALGLALNVPSSS 188

Db 121 HRSCPPGFGVQAGTPERTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180

QY 189 HDTLCTSCGFLPLSTRVPGAEE--CERAVIDF 218

Db 181 HDNI---CSGNSESTQKCGIDVTLCEAFRRF 209

## RESULT 6

US-09-042-785A-12

; Sequence 12, Application US/09042785A

; Patent No. 6194151

## GENERAL INFORMATION:

; APPLICANT: Busfield, Samantha J

; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042,785A  
; FILING DATE: 17-MAR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/938,896  
; FILING DATE: 26-SEP-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: MEI-001CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 401 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: Internal

US-09-042-785A-12

Query Match 27.2%; Score 444; DB 4; Length 401;

Best Local Similarity 39.6%; Pred. No. 3.6e-29;

Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps 4;

QY 11 LCLVLALPALLPVPAVRGVAET--PTYPRDAETGERLVCAQCPTGTFVQPCRRDST 68

Db 4 LCCAL---VFLDISIKWTQETFPKYLHYDEETSHQLLCKDCPPGTYLKQHCTAKWT 60

QY 69 TCGPCPPRHVTOFWNYLRCRYCNVLCGEREEARACHATHNRACRRTGFFAHAGFCLE 128

Db 61 VCAPCPDHYTDSWHTSDCLYCSPVKELQYVKQECNTRHNRVCECKEGRYLEIEFCLK 120

QY 129 HASCPPGAGVIAPGTPSQNTQCPQPPGTFSSSSSEQCPHRNCTALGLALNVPSSS 188

Db 121 HRSCPPGFGVQAGTPERTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180

QY 189 HDTLCTSCGFLPLSTRVPGAEE--CERAVIDF 218

Db 181 HDNI---CSGNSESTQKCGIDVTLCEAFRRF 209

## RESULT 7

US-08-795-445A-6

; Sequence 6, Application US/08795445A

; Patent No. 6284485

## GENERAL INFORMATION:

; APPLICANT: Boyle, William J.

; APPLICANT: Lacey, David L.

; APPLICANT: Calzone, Frank J.

; APPLICANT: Chang, Ming-Shi

; TITLE OF INVENTION: OSTEOPROTEGERIN

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-447A-6

      Query Match      27.2%; Score 444; DB 4; Length 401;
      Best Local Similarity 39.6%; Pred. No. 3.6e-29;
      Matches 84; Conservative 32; Mismatches 86; Indels 10; Gaps
      0

QY 11 LCLVLALPALLPVPVAVRGVAET--PTYPRDAETGERLVCACQPGTTFVQPRCRDSEP 68
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Db 4 LCCAL---VFLDISIKWTTQETFPKYLHYDEETSHQLLCDKCPGTVLKQHCTAKWKT 60

QY 69 TCGCPPRHRTQFNWYLERGRCYCNVLCGEREEEARACHATHNPACRCRTGFFAHAGFCLE 128
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Db 61 VCAPCPDHYTDSWHTSDCELYCSPVKELQYVQECNTHNVCVCKEGRVLETFCLK 120

QY 129 HASCPGAGVIAPGTSONTCQCPGPGTFSSASSSCQCPHRNCTALGLALNVPSSS 188
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Db 121 HRSCPFGVQVQAGTPERNTVCKRCPDGPFNSNETSKAPCRKHTNCSVFGLLLTQGNAT 180

QY 189 HDLTCTSGTGPISTRVPGAE--CERAVIDF 218
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Db 181 HDNI---CSGNSESTQKGDIVLTCEAEAFRF 209

RESULT 9
US-08-974-186-6
; Sequence 6, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53

```

```

ADDRESS: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-186-6
Query Match 27.2%: Score 444: DB 4: Length 401:

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Best Local Similarity   39.6%; Pred. No. 3.6e-29;
Matches    84; Conservative      32; Mismatches    86; Indels     10; Gaps         4;

QY       11  LLCLVLALPALLPVPAVRGVAET--PTYPWRDAETGERLVCAQCPPGTFFVORPCRRDSPT 68
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Db        4  LCCAL---VFLDISIKWTQTETFPFKYLHVDEETSQHLLCDKCPGGTYLKHCHTAKWKT 60
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QY       69  TCGCPCPRHHYTQFWNYLERCYCNWLGCEREEEARACHATHNCRACRTGFHAAGFCL 128
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Db       61  VCAPCPHYHTDSDHMTSDECLYCSPVKELQYVKQECNRTHRVCECKEGRYLEIEFLCK 120
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QY       129  HASCPPGAGVIAPTCTPSNTQOCPCPCTFSASSSSSEQCOPHRNCTALGLAINVPGSSS 188
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Db       121  HRS CPPGVVGQAQTPRGNTVKKRCPDGFTSNESRKAPCRKHTNCVSFGULLLTQQKNAT 180
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QY       189  HDTLCTSGTGPLSTRVPGAEE--CERAVIDF 218
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RESULT    10
US-08-795-446B-6
; Sequence 6, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; * CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,446B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-446B-6
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Query Match      27.2%  Score 444;  DB 4;  Length 401;
Best Local Similarity 39.6%;  pred. No. 3.6e-29;
Matches      84;  Conservative 33;  Mismatches 86;  Indels 10;  Gaps 4;

Qy  11  LLCVLALPALLPVPVGRVAET--PTYPWRDAETGERLVCAQCQPPGTFVQRPCRRDSPT 68
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Qy  69  TCGPCPPPHYTQFWNYLERGRCYNVLGCRBEEERACHATHINRACRGTGFHAAGFLE 128
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Db   61  VCAPCPDHYVTDSMHTSDECLYCSVPCKELOYVKQECNRTHNRYNRCCKEGRYLETFCLK 120
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[illegible]

RESULT 12

US-08-974-0

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; Sequence
; Patent No.

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; FACILE NO  
; GENERAL

; APPLIC

APPL. 19

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98. TITLE	98
99. TITLE	99
100. TITLE	100

NUMBER  
CORRECTION

; ADDI

; .  
STRI  
CITY

STA:

; count

ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974.022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-022-2

Query Match 26.0%; Score 425.5; DB 3; Length 401;  
Best Local Similarity 39.5%; Pred. No. 1.2e-27;  
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;  
QY 34 PTYPWRDAETGERLVCAOCPGTFVQRCRDRSPPTTCGCPPRHYTQFWNYLRCRYCNV 93  
DB 26 PKYLHYDPETGRLQCDKCAPGTLYLKQCHTVRRKTLVCPDPYSYDTSWHTSDECVYCS 85  
QY 94 LCGEREERACHATHNRACRRTGFFAHAGFCLHASCPCGAGVIAGTPTSONTCQPC 153  
DB 86 VCKELQTVKQECNRTHNRVCEEGRYLELEFCLHRSCPPGLVQLAGTPTERTVCKRC 145  
QY 154 PGFTSASSSECOQHNCRTALGLNVPGSSSHDILCTCTGFPPLSTRVPGAE--C 211  
DB 146 PDGFFSGTSSKAPCKKHTNCSSGLLLQKGNATHDNV---CSGNREATQNCGIDVTLC 202  
QY 212 ERAVIDFAFQDISIKRLQRLQAL 236  
DB 203 EEAFFFAVPTKLIIPNLSVLVDSL 227

RESULT 13  
US-08-795-445A-2  
Sequence 2, Application US/08795445A  
Patent No. 6284485  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795.445A  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-445A-2

Query Match 26.0%; Score 425.5; DB 4; Length 401;  
Best Local Similarity 39.5%; Pred. No. 1.2e-27;  
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;  
QY 34 PTYPWRDAETGERLVCAOCPGTFVQRCRDRSPPTTCGCPPRHYTQFWNYLRCRYCNV 93  
DB 26 PKYLHYDPETGRLQCDKCAPGTLYLKQCHTVRRKTLVCPDPYSYDTSWHTSDECVYCS 85  
QY 94 LCGEREERACHATHNRACRRTGFFAHAGFCLHASCPCGAGVIAGTPTSONTCQPC 153  
DB 86 VCKELQTVKQECNRTHNRVCEEGRYLELEFCLHRSCPPGLVQLAGTPTERTVCKRC 145  
QY 154 PGFTSASSSECOQHNCRTALGLNVPGSSSHDILCTCTGFPPLSTRVPGAE--C 211  
DB 146 PDGFFSGTSSKAPCKKHTNCSSGLLLQKGNATHDNV---CSGNREATQNCGIDVTLC 202  
QY 212 ERAVIDFAFQDISIKRLQRLQAL 236  
DB 203 EEAFFFAVPTKLIIPNLSVLVDSL 227

RESULT 14  
US-08-795-447A-2  
Sequence 2, Application US/08795447A  
Patent No. 6284728  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: Osteoprotegerin  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: One Angen Center Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91362-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795.447A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378D2  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-447A-2



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2002, 10:52:31 ; Search time 40.16 Seconds  
(without alignments)  
553.336 Million cell updates/sec

Title: US-09-280-567-2

Perfect score: 1634

Sequence: 1 MRALEGPGLSLCLVLALPA.....RVARMPGLRSVRERFLPVH 300

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1634	100.0	300	19 AAW66102	Amino acid sequenc
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3	1634	100.0	300	20 AAY03099	Human lung TNF-rec
4	1634	100.0	300	20 AAY42182	Human FLINT #1 pro
5	1634	100.0	300	20 AAY17479	Mammalian tumour n
6	1634	100.0	300	20 AAY06817	Human DCR3 polypep
7	1634	100.0	300	20 AAW97749	Human tumour necro
8	1634	100.0	300	20 AAW95082	Orphan receptor (H
9	1634	100.0	300	21 AAB19335	A full length huma
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21	1634	100.0	300	22 AAB48161	Human PRO212 poly
22	1634	100.0	300	22 AAB50903	Human PRO212 prote
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25	1619	99.1	300	21 AAB19710	Human Fas ligand 1
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29	1619	99.1	300	22 AAB68045	Amino acid sequenc
30	1619	99.1	300	22 AAB68048	Amino acid sequenc
31	1610	98.5	302	20 AAY42183	Human FLINT #2 pro
32	1509	92.4	300	21 AAB03623	Human Fas ligand 1
33	1502	91.9	300	21 AAB03622	Monkey Fas ligand
34	1502	91.9	300	21 AAB03624	Human Fas ligand 1
35	1491	91.2	271	20 AAY42184	Human mFLINT #1 pr
36	1491	91.2	271	21 AAB19334	A mature human Fas
37	1491	91.2	271	21 AAB19705	Human Fas ligand 1
38	1491	91.2	271	21 AAY97247	M88 TNF receptor r
39	1491	91.2	271	21 AAY96598	Human mature fas 1
40	1491	91.2	271	22 AAE03567	Human mature fas 1
41	1491	91.2	271	22 AAB68044	Amino acid sequenc
42	1491	91.2	271	22 AAB68047	Amino acid sequenc
43	1491	91.2	271	22 AAB74465	Human FLINT mature
44	1487	91.0	271	21 AAB19709	Protease-resistant
45	1487	91.0	271	22 AAE03571	Human mature fas 1

#### ALIGNMENTS

RESULT 1

AAW66102

ID AAW66102 standard; Protein; 300 AA.

XX

AC AAW66102;

XX

DT 02-DEC-1998 (first entry)

XX

DE Amino acid sequence of tumour necrosis related receptor (TR4).

XX

Human; tumour necrosis related receptor; TR4; agonist; antagonist;

KW Inhibition; chronic; acute; inflammation; arthritis; septicaemia;

KW autoimmune disease; transplant rejection; stroke; cancer;

KW Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN EP861850-A1.

XX

PD 02-SEP-1998.

XX

PF 20-JAN-1998; 98EP-0300382.

XX

PR 04-FEB-1997; 97US-0794796.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Emery J, Tan KB, Truneh A, Young PR;

XX

Human DCR3 polypep

XX

Human tumour necro

DR

Orphan receptor (H

XX

A full length huma

XX

New DNA encoding tumour necrosis related receptor - used to treat

PT and prevent e.g. inflammation, arthritis, septicaemia, autoimmune

PT diseases, transplant rejection, infection, stroke, ischaemia, ARDS,  
 XX restenosis, AIDS, bone disorders and cancer  
 PS Claim 1; Fig 1; 2lpp; English.

XX This is the amino acid sequence of the human tumour necrosis related  
 CC receptor (TR4), used in the method of the invention. The TR4 protein  
 CC or its agonist can be used to treat a subject in need of enhanced  
 CC TR4 polypeptide activity. The antagonist is used to inhibit TR4  
 CC polypeptide activity. The active agents can be used for the  
 CC treatment and prevention of diseases such as chronic and acute  
 CC inflammation, arthritis, septicemia, autoimmune diseases, transplant  
 CC rejection, stroke, cancer, Alzheimer's disease.

XX Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 19; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Qy 121 AHAGFCLHASCPPGAGVIAPGTPSQNTQCPCPGTFSASSSSSEQCPHNRCTALGLA 180  
 Db 121 ahagfclhascppgagviapgtpsqntqcpcpgtfsassssseqcqhnrctalgla 180  
 Qy 181 LNVPGSSSHDILCTSCGTFPLSTRVPGAEECERAVIDFVAFQDISIKRLQLQALEAPE 240  
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 Qy 241 GWGPTPRAGRAALQKLRRRLTELLGADGALLVRLQLQALVARMPLGLSVRRERFLPVH 300  
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# RESULT 2

AAW63622  
 ID AAW63622 standard; Protein; 300 AA.

AC AAW63622;

DT 26-OCT-1998 (first entry)

DE Human tumour necrosis factor receptor-6 alpha protein.

XX Human tumour necrosis factor receptor-6 alpha; TNFR-6 beta;  
 KW endothelial cells; keratinocytes; normal prostate; apoptosis;  
 KW prostate tumour tissue.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..30

FT Protein 31..300

FT FT /note= "TNFR-6 alpha"

FT Region 31..282

FT FT /note= "Soluble extracellular domain"

XX WO9830694-A2.

XX 16-JUL-1998.

PD 13-JAN-1998;

XX 98WO-US00153.

XX 14-JAN-1997;

XX 97US-0035496.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;

XX WPI; 1998-399142/34.

DR N-PSDB; AAV39085.

XX Human tumour necrosis factor receptors 6-alpha and 6-beta - used in  
 PT the diagnosis of immune system-related disorder(s)

XX Claim 20; Fig 1; 9lpp; English.

XX The present sequence represents the human tumour necrosis factor  
 CC receptor-6 alpha (TNFR-6 alpha) protein. The invention also provides  
 CC for the TNFR-6 beta protein (AAW63623). TNFR-6 alpha and TNFR-6 beta  
 CC are members of the tumour necrosis factor receptor (TNFR) family. TNFRs  
 CC are expressed in endothelial cells, keratinocytes, normal prostate and  
 CC prostate tumour tissue. For a number of disorders of these cells,  
 CC particularly of the immune system, substantially altered (whether  
 CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta  
 CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta  
 CC polypeptides, nucleic acids and antibodies are claimed to be useful in  
 CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and  
 CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are  
 CC also claimed to be useful for identifying ligands which may be useful  
 CC in the treatment of apoptosis related disorders.

XX Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 19; Length 300;

Best Local Similarity 100.0%; Pred. No. 7.4e-122;

Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALEGGLSLCLVLAIPALLPVPVGVAEPTTPYPRDAETGERLYCAQCPGTFVQR 60

Db 1 mralegpqlslclvialpallpvpvrgvaetpypvrdagetgerlyvcacqpgtfvqr 60

Qy 61 PCRRDSPPTCGPPRHYTQFNWYLCRYCNVLCGEREEERACHATHNRCRCRTGFF 120

Db 61 pcrrdspptcgprrhytqfwnylcrycnvlgereeeearachathnrcrcrtgff 120

Qy 121 AHAGFCLHASCPPGAGVIAPGTPSQNTQCPCPGTFSASSSSSEQCPHNRCTALGLA 180

Db 121 ahagfclhascppgagviapgtpsqntqcpcpgtfsassssseqcqhnrctalgla 180

Qy 181 LNVPGSSSHDILCTSCGTFPLSTRVPGAEECERAVIDFVAFQDISIKRLQLQALEAPE 240

Db 181 lnpvgssshdiltctscgtfplstrvpgaeeceraavidfvaqdisikrlqlqaleape 240

Qy 241 GWGPTPRAGRAALQKLRRRLTELLGADGALLVRLQLQALVARMPLGLSVRRERFLPVH 300

Db 241 gwgptpragraalqlkrrritellgagdgallvrlqlqalvarmpglsvrrerflpvh 300

# RESULT 3

AAW03099

ID AAY03099 standard; Protein; 300 AA.

AC AAY03099;

DT 09-DEC-1999 (first entry)

DE Human lung TNF-receptor protein.

XX Tumour necrosis factor; TNF; TNF receptor; human; lung; gene therapy;  
 KW detection; immunoassay; diagnosis; disease; immune system; tumour;  
 KW osteogenic system; cardiovascular system; central nervous system; asthma;  
 KW peripheral nervous systems; transplant incompatibility; antitumor;  
 KW rheumatoid arthritis; antiasthmatic; antiarthritic.

OS Homo sapiens.

XX







CC may also be used to identify specific binding proteins, potential  
 CC inhibitors. Antibodies against Dcr3 are used to treat cancer,  
 CC specifically of the lung and colon, also in diagnosis and for affinity  
 CC purification of the protein. Detecting mutations in the gene for Dcr3 is  
 CC also used to diagnose cancer, or predisposition to it. Dcr3 nucleic acid  
 CC is useful as hybridization probe to detect genomic or related sequences;  
 CC for chromosome and gene mapping; as source of antisense sequences; for  
 CC expression of recombinant Dcr3 and to generate transgenic animals (for  
 CC development and screening of therapeutic agents), also for in vivo or  
 CC ex vivo gene therapy.

XX Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 20; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALEGPGLSLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPTGFVQR 60  
 DB 1 mralepgglslclvlalpalpvpavrgvaetptypwrdaetgerlvcaqcpptgfvr 60  
 QY 61 PCRDSPTTCGPPRRHYTFQWNYLERCRYCNVLCGEREEERACHATHNRACRRTGFF 120  
 DB 61 pcrdspttcgpprrhytqfwnylerycnvlgereearachathnracrctgff 120  
 QY 121 AHAGFLEHASCPGAGVIAPGTPTSONTCQPCPPTFSASSSSSQCPHNRCTALGLA 180  
 DB 121 ahagflehscppgagvialpqtspntqtcpcpptsassssseqcqhnrctalgla 180  
 QY 181 LNVPGSSSHDTLTCTGTFPLSTRVPGAECERAVIDFVAFQDISIKRLQRLQALEAPE 240  
 DB 181 lnpvssshdtlctctgftplstrvpgaeceravidfvafqdisikrlqrlqaleape 240  
 QY 241 GWGPTPRAGRAALQKLRRRLTELLGAQDGLLVRLQALRVARMPGLERSVRERFLPVH 300  
 DB 241 gwgptpragraaalqklrrrltelligaqqdglvllqalrvarmpglersvrerflpvh 300

# RESULT 7

AAW97749  
 ID AAW97749 standard; Protein; 300 AA.

XX AAW97749;

DT 21-MAY-1999 (first entry)

XX Human tumour necrosis factor receptor ZTNFR-5.

XX ZTNFR-5; tumour necrosis factor receptor; TNFR; human;  
 KW cell maturation; bone cell regulation.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..23 /note= "signal peptide"  
 FT Protein 24..300 /note= "mature protein"  
 FT Domain 24..194 /note= "extracellular domain"  
 FT Region 49..71 /note= "cysteine-rich pseudo-repeat 1"  
 FT Region 72..113 /note= "cysteine-rich pseudo-repeat 1"  
 FT Region 114..151 /note= "cysteine-rich pseudo-repeat 1"  
 FT Region 152..194 /note= "cysteine-rich pseudo-repeat 1"

XX WO9904001-A1.

XX 28-JAN-1999.

PD

XX

PF 21-JUL-1998; 98WO-US15072.

XX 21-JUL-1997; 97US-0053203.

XX (ZYMO ) ZYMOGENETICS INC.

XX Farrah TM;

XX WPI; 1999-132245/11.

XX N-PSDB; AAX07226.

XX Novel tumour necrosis factor receptor ZTNFR5 - useful for  
 PT regulating maturation of TNF-ligand bearing cells  
 PS Claim 1; Page 84-85; 109pp; English.

XX This polypeptide comprises a new, secreted tumour necrosis factor  
 CC receptor (see AAW97749), designated ZTNFR-5. Novel ZTNFR-5 encoding  
 CC polynucleotides and polypeptides were initially identified by  
 CC querying an expressed sequence tag (EST) database for sequences  
 CC homologous to conserved motifs within the TNF receptor family.  
 CC Based on this search, a contig of 16 ESTs (see AAX07226) was  
 CC constructed. ZTNFR-5 polypeptides comprise 4 cysteine-rich repeats  
 CC (see also AAW97750-55) that are homologous to other TNF receptors, in  
 CC particular the soluble, secreted TNF receptor osteoprotegerin.  
 CC ZTNFR-5 polypeptide can be prepared by recombinant methods. The  
 CC polypeptide, especially the extracellular domain, can be used to  
 CC generate a soluble variant of ZTNFR-5. The polypeptides and  
 CC nucleic acids can be used to screen for ligands, agonists and  
 CC antagonists of ZTNFR-5. The polypeptides can be used in bone cell  
 CC regulation and to regulate the maturation of TNF ligand-bearing  
 CC cells such as T- or B-cells, lymphocytes, peripheral blood  
 CC mononuclear cells, polymorphonuclear leukocytes, fibroblasts or  
 CC haematopoietic cells.  
 XX Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 20; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALEGPGLSLCLVLALPALLPVPVAVRGVAETPTYPWRDAETGERLVCAQCPTGFVQR 60

DB 1 mralepgglslclvlalpalpvpavrgvaetptypwrdaetgerlvcaqcpptgfvr 60

QY 61 PCRDSPTTCGPPRRHYTFQWNYLERCRYCNVLCGEREEERACHATHNRACRRTGFF 120

DB 61 pcrdspttcgpprrhytqfwnylerycnvlgereearachathnracrctgff 120

QY 121 AHAGFLEHASCPGAGVIAPGTPTSONTCQPCPPTFSASSSSSQCPHNRCTALGLA 180

DB 121 ahagflehscppgagvialpqtspntqtcpcpptsassssseqcqhnrctalgla 180

QY 181 LNVPGSSSHDTLTCTGTFPLSTRVPGAECERAVIDFVAFQDISIKRLQRLQALEAPE 240

DB 181 lnpvssshdtlctctgftplstrvpgaeceravidfvafqdisikrlqrlqaleape 240

QY 241 GWGPTPRAGRAALQKLRRRLTELLGAQDGLLVRLQALRVARMPGLERSVRERFLPVH 300

DB 241 gwgptpragraaalqklrrrltelligaqqdglvllqalrvarmpglersvrerflpvh 300

# RESULT 8

AAW95082

ID AAW95082 standard; Protein; 300 AA.

XX AAW95082;

XX 20-MAY-1999 (first entry)

XX Orphan receptor (HUMAN NTR-1) polypeptide.

DE

XX HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;  
 KW tumour necrosis factor receptor; muscle disorder; bone mass; screening;  
 KW muscle metabolism; binding agent; cognate ligand.  
 XX  
 OS Homo sapiens.  
 XX WO9907738-A2.  
 PN  
 PD 18-FEB-1999.  
 XX  
 XX 04-AUG-1998; 98WO-US16202.  
 PF  
 XX 06-AUG-1997; 97US-0054869.  
 PR  
 XX (PROC ) PROCTER & GAMBLE CO.  
 PA (REGE-) REGENERON PHARM INC.  
 XX  
 XX Masiakowski PJ, Morris J, Valenzuela DM;  
 PI WPI; 1999-167365/14.  
 XX  
 DR N-PSDB; AAX22300.  
 XX  
 XX Novel orphan human receptor polypeptide and nucleic acid - useful as  
 PT diagnostic reagents and for treatment of muscle disorders  
 PT  
 PS Claim 7; Page 21; 23pp; English.  
 XX  
 XX This represents a HUMAN NTR-1 polypeptide, a novel orphan receptor. The  
 CC protein is related to osteoprotegerin (OPG) and to tumour necrosis factor  
 CC receptor (TNFR). Host cells transfected with a vector comprising the  
 CC HUMAN NTR-1 nucleic acid are used for the recombinant expression of the  
 CC protein. HUMAN NTR-1 proteins and antibodies immuno specific for the  
 CC protein are useful for diagnosis and treatment of humans and animals,  
 CC especially muscle disorders, as the receptor is involved in regulation of  
 CC bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful  
 CC for screening for novel binding agents, and cognate ligands, which may be  
 CC used to treat disorders associated with HUMAN NTR-1 imbalance.  
 XX  
 XX Sequence 300 AA:  
 SQ  
 Query Match 100.0%; Score 1634; DB 20; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRALGPGLSLCLVLPALLPVPVAVRGVAETPTYPWRDAETGERLYCAQCPPGTFVQR 60  
 DB 1 mraleppglsllclvlalpallvpvavrgvaetptyprdaetgerlyvcaqcpptfvqr 60  
 QY 61 PCRDSPTTCGPPRRHYTQFWNYLCRCYCNVLCGEREEERACHATHNRACRRTGFF 120  
 DB 61 pcrdspttcgpprrhytqfwnylercrycnvlgereeeearachathnrcrctrtgff 120  
 QY 121 AHAGFCLHASCPGAGVIAPGTPSQNTQCPPTGTFSSSSSEQCQPHRNCTALGIA 180  
 DB 121 ahagfclhascpagviapgtpsqntqcpptgtsassssseqcqphrncnctalgia 180  
 QY 181 LNVPGSSSHDTLCTCTGTFPLSTRVPGAECERAVIDFVAFODISIKRLORLLOALEAPE 240  
 DB 181 lnvpgssshdtlctctgtfplstrvpgaeceravidfvafodisikrlqrlloaleape 240  
 QY 241 GWGPTPRAGRAALQLKRRRLTELLGADGALLVRLLOALVARMPGLRSVRERFLPVH 300  
 DB 241 gwgptpragraalqlkrrrltellgagdgallvrlloalvarmpglersvrerflpvh 300  
 RESULT 9  
 AAB19335  
 ID AAB19335 standard; Protein; 300 AA.  
 XX  
 AC AAB19335;  
 XX

DT 19-FEB-2001 (first entry)  
 XX  
 DE A full length human FAS Ligand Inhibitory Protein (FLINT).  
 XX  
 KW Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;  
 KW tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;  
 KW acute respiratory distress syndrome; ulcerative colitis;  
 KW chronic obstructive pulmonary disease; Crohn's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200038465-A2.  
 XX  
 PD 05-OCT-2000.  
 XX  
 XX 20-MAR-2000; 2000WO-US06417.  
 PF  
 XX 30-MAR-1999; 99US-0126839.  
 PR 21-JUN-1999; 99US-0140077.  
 PR 21-JUN-1999; 99US-0140156.  
 PR 20-OCT-1999; 99US-0160566.  
 PR 18-FEB-2000; 2000US-0183398.  
 XX  
 XX (ELIL ) LILLY & CO ELI.  
 PA  
 XX Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micanovic R;  
 PI Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Witcher DR;  
 PI Wroblewski VJ;  
 XX  
 XX WPI; 2000-656167/63.  
 DR  
 XX FAS Ligand Inhibitory Protein analogs useful for treating abnormal  
 PT apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,  
 PT chronic obstructive pulmonary disease ulcerative colitis or Crohn's  
 PT disease  
 XX  
 PS Disclosure: Page 113-114; 114pp; English.  
 XX  
 CC The present sequence represents a full length human FAS Ligand Inhibitory  
 CC protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor  
 CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature  
 CC FLINT protein is modified to produce analogues, which have greater  
 CC potency, longer in vivo half-lives, decreased aggregation, decreased  
 CC absorption onto surfaces, increased solubility and improved ease of  
 CC formulation. The FLINT analogue is useful for treating a patient  
 CC suffering from disease or condition relating to abnormal apoptosis such  
 CC as acute lung injury, acute respiratory distress syndrome, pulmonary  
 CC fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or  
 CC Crohn's disease.  
 XX  
 SQ Sequence 300 AA;  
 Query Match 100.0%; Score 1634; DB 21; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-122;  
 Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRALGPGLSLCLVLPALLPVPVAVRGVAETPTYPWRDAETGERLYCAQCPPGTFVQR 60  
 DB 1 mraleppglsllclvlalpallvpvavrgvaetptyprdaetgerlyvcaqcpptfvqr 60  
 QY 61 PCRDSPTTCGPPRRHYTQFWNYLCRCYCNVLCGEREEERACHATHNRACRRTGFF 120  
 DB 61 pcrdspttcgpprrhytqfwnylercrycnvlgereeeearachathnrcrctrtgff 120  
 QY 121 AHAGFCLHASCPGAGVIAPGTPSQNTQCPPTGTFSSSSSEQCQPHRNCTALGIA 180  
 DB 121 ahagfclhascpagviapgtpsqntqcpptgtsassssseqcqphrncnctalgia 180  
 QY 181 LNVPGSSSHDTLCTCTGTFPLSTRVPGAECERAVIDFVAFODISIKRLORLLOALEAPE 240  
 DB 181 lnvpgssshdtlctctgtfplstrvpgaeceravidfvafodisikrlqrlloaleape 240

QY 241 GWGPTPRAGRAALQKLRRRLTELLGAQDQALLVRLQLALRVARMPGLSRRERFLPVH 300  
DB 241 gwgptpragraalqklrrrltellgaqdgallvrlqlalrvarmpglsrrerflpvh 300

RESULT 10  
AAB28559  
ID AAB28559 standard; protein: 300 AA.  
XX  
AC AAB28559;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human soluble TNF receptor tnfr1-1.  
XX  
KW Human; tumour necrosis factor like-1; TNFL1; tumour necrosis factor; TNF;  
KW immunosuppressive; antiarthritic; neuroprotective; dermatological;  
KW antinflammatory; antidiabetic; cytostatic; osteopathic; gene therapy;  
KW colon cancer; rheumatoid arthritis; septic shock; Crohn's disease;  
KW osteoporosis; autoimmune disease; myasthenia gravis;  
KW insulin-dependent diabetes mellitus.  
XX  
OS Homo sapiens.  
XX  
PN WO200060079-A2.  
XX  
PD 12-OCT-2000.  
XX  
PF 05-APR-2000; 2000WO-US09058.  
XX  
PR 05-APR-1999; 99US-0286529.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
PI Tribouley C;  
XX  
XX WPI; 2000-665004/64.  
DR N-PSDB; AAC63764.  
XX  
XX Tumour necrosis factor (TNF) and TNF receptor superfamily protein  
PT members TNFR-L and TNFR-L, useful for enhancing or decreasing TNF  
PT activities such as inducing cell death and lymphoid organogenesis  
XX  
PS Claim 1; Page 72; 77pp; English.  
XX  
CC The present sequence is given in a specification relating to an isolated  
CC human protein designated tumour necrosis factor like-1 (TNFL1). It may be  
CC used to induce cell death in tumours, to induce apoptosis of activated T  
CC cells, to induce inflammation, and to rescue resting T cells from  
CC apoptosis. TNF receptors are used to regulate the function of a TNF  
CC ligand which plays a role in apoptosis, inflammation, differentiation, or  
CC proliferation. Expression of the receptors can also be useful as markers  
CC for cancer, especially for colon cancer. Diseases which can be treated  
CC using ligands and/or receptors of the TNF/TNFR superfamily include  
CC rheumatoid arthritis, cancer, septic shock, Crohn's disease and  
CC osteoporosis. The polynucleotides can be used in gene delivery vehicles,  
CC for the purpose of delivering a mRNA or oligonucleotide, full-length  
CC protein, fusion protein, polypeptide, or ribozyme, or single-chain  
CC antibody, into a cell. The newly identified receptor proteins play  
CC regulatory roles in cell proliferation and/or differentiation. The  
CC receptors can also play a role in the negative regulation of  
CC osteoclastogenesis. Soluble TNFR-like receptors can be useful in the  
CC neutralisation of TNF or TNF-like ligands. A TNF-L protein can also be  
CC used to treat autoimmune diseases (myasthenia gravis and  
CC insulin-dependent diabetes mellitus), tumours, and proliferative  
CC disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be  
CC delivered to subjects for the purpose of screening test compounds for  
CC those which are useful for enhancing transfer of TNF-L subgenomic  
CC polynucleotides to the cell or for enhancing subsequent biological  
CC effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell.  
XX  
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;  
Best Local Similarity 100.0%; Pred. No. 7.4e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALEGPGLSLLCLVLALPVPVAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVOR 60  
DB 1 mralepgpglsllclvlalpvpavrgvaetptyprwdaetgerlvcaqcpptfivr 60

QY 61 PCRDSPTTCGCPPRHYTFWNLYLRCRYCNVLCGEREEARACHATHNRACRGTGFF 120  
DB 61 pcrdspttcgcpprhytfnwlylrcrycnvlgereearachathnrcrctgff 120

QY 121 AHAGCFLHASCPGAGVIAPGTSPONTQCPGCTFSASSSSSQCPHNRCTALGIA 180  
DB 121 ahagcflhascpagviapgtspontqcpctfsassssqcpnhnrcntalgia 180

QY 181 LNVPGSSSHDTLCTCTGFPPLSTRVPGAECEERAVDFVAFODISIKRLQLQALEAPE 240  
DB 181 lnvpgssshdtlctctgfpplstrvpgaeeceravldfvafodisikrllqaleape 240

QY 241 GWGPTPRAGRAALQKLRRRLTELLGAQDQALLVRLQLALRVARMPGLSRRERFLPVH 300  
DB 241 gwgptpragraalqklrrrltellgaqdgallvrlqlalrvarmpglsrrerflpvh 300

RESULT 11  
AAB24057  
ID AAB24057 standard; Protein: 300 AA.  
XX  
AC AAB24057;  
XX  
DT 29-JAN-2001 (first entry)  
XX  
DE Human PRO212 protein sequence SEQ ID NO:2.  
XX  
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
KW proliferation; tumorigenesis; identification; cancer; cytostatic;  
KW nocrotic; neuroprotective; antiinflammatory; immunosuppressive;  
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;  
KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;  
KW hypothalamic disorder; glandular disorder; macrophagal disorder;  
KW epithelial disorder; stromal disorder; blastocoealic disorder;  
KW inflammatory disorder; immunologic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200053755-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 06-JAN-2000; 2000WO-US00376.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 07-JUL-1999; 99US-0143048.  
PR 26-JUL-1999; 99US-0145698.  
PR 30-NOV-1999; 99WO-US28313.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
PI Watanabe CK, Wood WT;  
XX  
XX WPI; 2000-572270/53.  
DR N-PSDB; AAC58367.  
XX  
PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
PT treatment, diagnosis and prevention of cancer -  
XX



CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
CC autoimmune or immune-mediated skin diseases, allergic diseases,  
CC immunological diseases of the lung, and transplantation associated  
CC diseases including graft rejection and graft-versus-host-disease.  
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;  
Best Local Similarity 100.0%; Pred. No. 7.4e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALEGPGLSLCLVLALPALLPVPVAVRGVAETPTVPRDAETGERLVCAQCPTGTFVOR 60  
|||||  
Db 1 mralegpglsllclvlalpallpvpavrgvaetptvprdaetgerlvcaqcpptgfvr 60

QY 61 PCRRDSPPTTCGPPRRHYTFQWNYLRCRYCNVLCGEREEARACHATHNRACRCRTGFF 120  
|||||  
Db 61 pccrrdsppttcgpprrhytfqwnylercrycnvlgereearachathnrcrcrtgff 120

QY 121 AHAGFCLEHASCPPGAGVIAPGTPSONTCQCPPTGTFSSASSSSSQCPHNRCTALGLA 180  
|||||  
Db 121 ahagfclchascppgagviapgtpsontcqcpptgfsasssssqcqhnrctalgla 180

QY 181 LNVPGSSSHDTLCTCTGCPPLSTRVPGAECERAVIDFAFQDISIKRLQRLQALEAPE 240  
|||||  
Db 181 lnvpgssshdtlctctgcpplstrvpgaeceravidfafqdisikrlqlqaleape 240

QY 241 GWGPTPRAGRAALQKLRRRLTELLGAQDALLVRLQLALRVARMPGLERSVRERFLPVH 300  
|||||  
Db 241 gwgptpragraaalqklrrrltellgaqgallvrlqlalrvarmpglersvrerflpvh 300

RESULT 13  
AAB03621  
ID AAB03621 standard; Protein: 300 AA.  
XX  
AC AAB03621;  
XX  
DT 03-JAN-2001 (first entry)  
XX  
DE Human Fas ligand inhibitor FLINT.  
XX  
KW Human; Fas ligand inhibitor; FLINT: apoptosis; autoimmune disease;  
KW inflammation; infectious disease; ischaemia; Alzheimer's disease;  
KW Parkinson's disease; Crohn's disease; transplantation.  
XX  
OS Homo sapiens.

Key Location/Qualifiers  
FT Peptide 1..29 /label= signal\_peptide  
FT Protein 30..300 /label= mature\_FLINT  
FT Domain 1..42 /label= domain\_1  
FT Domain 43..85 /label= domain\_2  
FT Domain 86..122 /label= domain\_3  
FT Domain 123..165 /label= domain\_4  
FT

XX WO200034782-A1.  
PN 15-JUN-2000.  
XX  
XX 07-DEC-1999; 99WO-US28696.  
PF  
PR 09-DEC-1998; 98US-0111575.  
PR 09-DEC-1998; 98US-0111580.  
PR 07-JAN-1999; 99US-0115069.  
XX  
PA (ELIL ) LILLY & CO ELI.  
XX  
PI Rosteck PRJ, Song HY, Su EW;  
XX  
DR WPI; 2000-431379/37.  
DR N-PSDB; AAA53208.  
XX  
XX Novel monkey Fas ligand inhibitor polypeptides, useful for treating  
PT inflammatory or autoimmune disease such as rheumatoid arthritis,  
PT infectious diseases such as chronic hepatitis, and  
PT ischaemia/Re-perfusion conditions -  
XX  
XX Claim 19; Page 91-93; 101pp; English.  
XX  
CC The present sequence is the protein sequence of the human Fas ligand  
CC inhibitor (FLINT). The FLINT protein is involved in cell-specific  
CC apoptosis, and can be used to treat inflammatory and autoimmune diseases  
CC such as rheumatoid arthritis, inflammatory bowel disease,  
CC graft-versus-host disease, diabetes, psoriasis and Graves' disease,  
CC infectious diseases such as HIV-induced lymphopenia, fulminant viral  
CC hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated  
CC ulceration, ischaemia and reperfusion conditions including acute  
CC myocardial infarction, acute coronary syndrome, congestive heart failure  
CC and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung  
CC injury and acute respiratory distress syndrome, Crohn's disease, brain  
CC trauma and injury, chronic glomerulonephritis, osteoporosis, aplastic  
CC anaemia, myelodysplasia, ulcerative colitis, Down's syndrome, and  
CC multiple sclerosis. In addition, the protein and its gene can be used to  
CC prevent apoptosis following organ transplantation.  
XX  
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;  
Best Local Similarity 100.0%; Pred. No. 7.4e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALEGPGLSLCLVLALPALLPVPVAVRGVAETPTVPRDAETGERLVCAQCPTGTFVOR 60  
|||||  
Db 1 mralegpglsllclvlalpallpvpavrgvaetptvprdaetgerlvcaqcpptgfvr 60

QY 61 PCRRDSPPTTCGPPRRHYTFQWNYLRCRYCNVLCGEREEARACHATHNRACRCRTGFF 120  
|||||  
Db 61 pccrrdsppttcgpprrhytfqwnylercrycnvlgereearachathnrcrcrtgff 120

QY 121 AHAGFCLEHASCPPGAGVIAPGTPSONTCQCPPTGTFSSASSSSSQCPHNRCTALGLA 180  
|||||  
Db 121 ahagfclchascppgagviapgtpsontcqcpptgfsasssssqcqhnrctalgla 180

QY 181 LNVPGSSSHDTLCTCTGCPPLSTRVPGAECERAVIDFAFQDISIKRLQRLQALEAPE 240  
|||||  
Db 181 lnvpgssshdtlctctgcpplstrvpgaeceravidfafqdisikrlqlqaleape 240

QY 241 GWGPTPRAGRAALQKLRRRLTELLGAQDALLVRLQLALRVARMPGLERSVRERFLPVH 300  
|||||  
Db 241 gwgptpragraaalqklrrrltellgaqgallvrlqlalrvarmpglersvrerflpvh 300

RESULT 14  
AAY97246  
ID AAY97246 standard; Protein: 300 AA.  
XX

AA97246;  
19-DEC-2000 (first entry)  
M68 TNF receptor related protein.  
M68; tumour necrosis factor; TNF; programmed cell death; apoptosis; receptor; immune response; cell differentiation; ligand; cancer; bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis; Grave's disease; idiopathic myxodema; autoimmune diabetes; thrombotic thrombocytopenic purpura; multiple sclerosis; liver diseases; autoimmune gastritis; ulcerative colitis; glomerulonephritis; pulmonary fibrosis; heart failure; atherosclerosis; aplastic anaemia; myelodysplastic syndromes; osteoporosis; Alzheimers disease; Parkinsons disease; stroke; myocardial infarction; human.  
Homo sapiens.  
WO200046247-A1.  
10-AUG-2000.  
04-FEB-2000; 2000WO-US03037.  
05-FEB-1999; 99US-0118902.  
20-DEC-1999; 99US-0172754.  
(MERI ) MERCK & CO INC.  
Ba1 C;  
WPI; 2000-506066/45.  
N-PSDB; AAA53800, AAA53801, AAA53802.  
Isolated human M68 nucleic acids and proteins which are part of the tumor necrosis factor receptor (TNFR) family, useful for identifying modulators that may be used to treat various diseases e.g. cancer, osteoporosis, Alzheimer's disease  
Claim 1; Page 75-76; 80pp; English.  
The M68 protein is a member of a family of proteins which have roles in immune responses, cell death, cell proliferation and stimulation of cell differentiation. M68 lacks a transmembrane domain and is a secreted factor suggesting that it functions as a natural inhibitor for its ligand. The altered expression pattern of M68 in a multitude of tissues suggests that M68 may play a role in cancer by binding to its ligand and blocking apoptotic cell death induced by such a ligand. This anti-apoptotic role of M68 suggests that modulators of M68 will be useful in treatment of apoptosis-related diseases such as various forms of cancer and various bone disorders. M68 nucleic acids and proteins are therefore useful for treating conditions involving atypical apoptosis and for identifying modulators of M68. Modulators of M68 are useful for treatment of cancer and other diseases associated with abnormal levels of apoptosis including systemic lupus erythematosus, Hashimoto's thyroiditis, Grave's disease, idiopathic myxodema, autoimmune diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis, liver diseases, autoimmune gastritis, ulcerative colitis, glomerulonephritis, pulmonary fibrosis, heart failure, atherosclerosis, aplastic anaemia, myelodysplastic syndromes, osteoporosis, Alzheimers disease, Parkinsons disease, stroke, and myocardial infarction.  
Sequence 300 AA;  
Query Match 100.0%; Score 1634; DB 21; Length 300;  
Best Local Similarity 100.0%; Pred. No. 7.4e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRALEGGPGLSLCLVLPALLPVPVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Db 1 mraleppglslclvlpallpvpvrigvaetpypwrdaetgerlvcaqppgtfvqr 60  
QY 61 PCRRDSPPTTCGCPPRHYTFQWNYLERCRYCNVLCGEREEERACHATHNRCRCRTGFF 120  
Db 61 pcrdspttcgcpprhytqfwnylercrycnvlgereeeearachathnrcrcrtgff 120  
QY 121 AHAGFCLHASCPPGAGVIAPGTPTSONTCQCPPTGTFSSSSSSQCPHNRCTALGLA 180  
Db 121 ahagfclhascppgagviapgtptsqntcpcppgtfssssssqcpqhnrctalgla 180  
QY 181 LNPVSSSHDTLCTCTGFPPLSTRVPGAECEERAVIDFVAFQDISIKRLQLLALEAPE 240  
Db 181 lnpvssshdtlctctgfpplstrvpgaeceeravidfvafqdisikrlqllqaleape 240  
QY 241 GNGPFRAGRAALQLKLRRLTELLCAQDQALLVRLQLALRVARMPGLERSVRERLPVH 300  
Db 241 gngpfragraalqlklrrltellgaqdgallvrlqlalrvarmpglersvrerlpvh 300  
RESULT 15  
AA90357  
ID AAY90357 standard; Protein; 300 AA.  
XX  
AC AAY90357;  
XX  
DT 04-DEC-2000 (first entry)  
XX  
DE Human tumour necrosis factor receptor-6 alpha protein sequence.  
XX  
KW Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;  
KW ocular neovascularisation; solid tumour; malignancy; prostate cancer;  
KW breast cancer; colon cancer; diabetic retinopathy; microbial infection;  
KW pre-maturity macular degeneration; allergy; inflammation; tissue damage;  
KW thyroid associated ophthalmopathy; cell damage; parasitic infection;  
KW bone disease; osteoporosis; atherosclerosis; cardiovascular disease;  
KW neurodegenerative disorder; Alzheimer's disease; immune disorder;  
KW graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;  
KW psoriasis; septic shock; ulcerative colitis; therapy.  
XX  
OS Homo sapiens.  
XX  
XX WO200052028-A1.  
XX  
PD 08-SEP-2000.  
XX  
PF 03-MAR-2000; 2000WO-US05686.  
XX  
PR 04-MAR-1999; 99US-0121774.  
PR 12-MAR-1999; 99US-0124092.  
PR 27-APR-1999; 99US-0131279.  
PR 30-APR-1999; 99US-0131964.  
PR 02-AUG-1999; 99US-0146371.  
PR 01-DEC-1999; 99US-0168235.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Gentz RL, Ni J, Ebner R, Yu G, Ruben SM, Feng P;  
XX  
DR WPI; 2000-572174/53.  
DR N-PSDB; AAA37772.  
XX  
PT Nucleic acids encoding human tumour necrosis factor receptor (TNFR)  
PT proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g.  
PT Alzheimer's disease, osteoporosis and graft rejection -  
XX  
PS Claim 20; Fig 1; 332pp; English.  
XX  
CC This sequence represents the human tumour necrosis factor receptor 6  
CC alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA  
CC and protein sequences can be used in the prevention, treatment and  
CC diagnosis of diseases associated with inappropriate TNFR expression. The  
CC nucleic acids, polypeptides, antibodies, agonists and antagonists against

CC them may be used for the treatment of a range of conditions such as  
CC disorders associated with neovascularisation (especially ocular  
CC neovascularisation) (such as solid tumours and malignancies (e.g.  
CC prostate cancer, breast cancer and colon cancer), diabetic retinopathy  
CC and pre-maturity macular degeneration), allergies, inflammation,  
CC thyroid associated ophthalmopathy tissue/cell damage, wounds, microbial  
CC and parasitic infections, bone disease (e.g. osteoporosis),  
CC atherosclerosis, pain, cardiovascular disease (e.g. stroke),  
CC neurodegenerative disorders (e.g. Alzheimer's disease), immune  
CC disorders (e.g. graft rejection), rheumatism, liver disease,  
CC autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative  
CC colitis.  
XX  
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;  
Best Local Similarity 100.0%; Pred. No. 7.4e-122;  
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRALEGSLCLVLPAVPAVGVAEPTYPWRDAETGERLVCAQCPPGTFVQR 60  
Db 1 mraleggslclclvlpavpavgaetpypwrdaetgerlvcaqcpptfvqr 60

QY 61 PCRDSPTTCGPPPHYTFWNYLERCRYCNVLCGEREEERACHATHNRACRCRTGFF 120  
Db 61 pcrdspttcgppphrhytfwnylercrycnvlgereeeearachathnracrcrtgff 120

QY 121 AHAGFLEHASCPPGAGVIAPGTPSONTCQPCPGTFSASSSSSQCPHRNCTALGLA 180  
Db 121 ahagflehascppgagviapgtpsqntcqcpcpgtfsassssseqcphrncnctalgla 180

QY 181 LNVPGSSSHDTLCTSGTGFPLSTRVPGAEECEERAVIDFVAFQDISIKRLQRLQALEAPE 240  
Db 181 lnvpgssshdtlctsgtgpplstrvpgaeeceeravidfvafqdisikrlqllqaleape 240

QY 241 GWGPTPRAGRAALQLKRLRLTELLGAQDQALLVRLLOALRVARMPGLERSVRERFLPVH 300  
Db 241 gwgptpragraalqlkrrrlteligaqdqallvrlloalrvarmpglrsvrerflpvh 300

Search completed: May 10, 2002, 10:53:49  
Job time: 78 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 10, 2002, 10:59:02 ; Search time 40.93 seconds

(without alignments)  
968.478 Million cell updates/sec

Title: US-09-280-567-6

Perfect score: 1491

Sequence: 1 VAETPTYPWRDAETGERLVC.....RVARMPGLERSVRFELFVH 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.17.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1491	100.0	300	4	O95407
2	440.5	29.5	372	4	Q9UHP4
3	440.5	29.5	401	4	O00300
4	425.5	28.5	401	11	O08727
5	424.5	28.5	401	11	O08712
6	395	26.5	302	13	Q9PUS0
7	338.5	22.7	425	4	Q16042
8	333.5	22.4	459	11	Q62327
9	327	21.9	482	11	O88734
10	297	19.9	630	13	Q98SM6
11	288.5	19.3	655	11	Q9EPU5
12	287	19.2	655	4	O75509
13	275	18.4	348	12	O57277
14	275	18.4	348	12	O57103
15	275	18.4	348	12	O57108
16	270.5	18.1	349	12	O57100
17	268.5	18.0	349	12	O57291
18	268.5	18.0	349	12	O57101
19	268.5	18.0	349	12	O57102

20	267.5	17.9	349	12	O57099	O57099 monkeypox v
21	260	17.4	348	12	O57112	O57112 variola vir
22	260	17.4	348	12	O85407	O85407 variola vir
23	260	17.4	349	12	O57110	O57110 variola vir
24	260	17.4	349	12	O57111	O57111 variola vir
25	260	17.4	349	12	O89118	O89118 variola vir
26	260	17.4	349	12	O89098	O89098 variola vir
27	260	17.4	350	12	O57116	O57116 cowpox viru
28	259	17.4	360	12	O57118	O57118 cowpox viru
29	258.5	17.3	355	12	O85308	O85308 cowpox viru
30	257.5	17.3	326	12	O57120	O57120 cowpox viru
31	257.5	17.3	349	12	O57284	O57284 camelpox vi
32	257.5	17.3	349	12	O57098	O57098 camelpox vi
33	254.5	17.1	326	12	O57122	O57122 cowpox viru
34	254.5	17.1	351	12	O73559	O73559 cowpox viru
35	253.5	17.0	349	12	O57305	O57305 cowpox viru
36	253.5	17.0	349	12	O57097	O57097 camelpox vi
37	253.5	17.0	351	12	O57117	O57117 cowpox viru
38	252	16.9	349	12	O57109	O57109 variola vir
39	251	16.8	347	12	O57119	O57119 cowpox viru
40	249.5	16.7	347	12	O57115	O57115 cowpox viru
41	248.5	16.7	351	12	O57121	O57121 cowpox viru
42	245.5	16.5	350	12	O57123	O57123 cowpox viru
43	244	16.4	283	6	Q9XSZ8	Q9XSZ8 cercopithec
44	235.5	15.8	616	4	Q9Y6Q6	Q9Y6Q6 homo sapien
45	230.5	15.5	276	13	Q9DDDD2	Q9DDDD2 gallus gall

## ALIGNMENTS

RESULT	ID	PRELIMINARY;	PRT;	300 AA.
O95407	O95407	AC	O95407;	
DT	O1-MAY-1999	(Tremblrel. 10, Created)		
DT	O1-MAY-1999	(Tremblrel. 10, Last sequence update)		
DT	O1-JUN-2001	(Tremblrel. 17, Last annotation update)		
DE	DECOY RECEPTOR 3 (M68)	(M68C) (M68E) (DJ583P15.1.1).		
GN	DCR3 OR TR6 OR TNFRSF6B.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-99087326; PubMed-9872321;			
RA	Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,			
RA	Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,			
RA	Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,			
RA	Goddard A.D., Botstein D., Ashkenazi A.;			
RT	"Genomic amplification of a decoy receptor for Fas ligand in lung and			
RT	colon cancer."			
RL	Nature 396:699-703(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=BLOOD;			
RC	MEDLINE-99253915; PubMed-10318773;			
RA	Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;			
RT	"A newly identified member of tumor necrosis factor receptor			
RT	superfamily (TR6) suppresses LIGHT-mediated apoptosis."			
RL	J. Biol. Chem. 274:13733-13736(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PANCREAS;			
RX	MEDLINE-20122600; PubMed-10655513;			
RA	Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,			
RA	Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.F.;			
RT	"Overexpression of M68/DCR3 in human gastrointestinal tract tumors			
RT	Independent of gene amplification and its location in a four-gene			
RT	cluster."			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).			
RN	[4]			



CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
 CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY  
 CC SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,  
 CC KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN  
 CC A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN  
 CC THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC EMBL: AB002146; BAA25910.1; -.  
 CC EMBL: AB008822; BAA32076.1; -.  
 CC EMBL: AB008821; BAA32076.1; JOINED.  
 CC EMBL: U94332; AAB53709.1; -.  
 CC HSSP: P25942; ICDF.  
 CC MIM: 602643; -.  
 CC InterPro: IPR000488; Death.  
 CC InterPro: IPR001368; TNFR\_c6.  
 CC Pfam: PF00020; TNFR\_c6; 3.  
 CC ProDom: PD000771; TNFR\_c6; 1.  
 CC SMART: SM00005; DEATH; 1.  
 CC SMART: SM00208; TNFR; 4.  
 CC PROSITE: PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 CC PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 CC Glycoprotein; Repeat; Cytokine; Signal.  
 CC SIGNAL 1 21 BY SIMILARITY.  
 CC CHAIN 22 401 OSTEOPROTEGERIN.  
 CC DOMAIN 23 63 4 X TNFR-CYS.  
 CC REPEAT 23 63  
 CC REPEAT 107 143 TNFR-CYS 1.  
 CC REPEAT 107 143 TNFR-CYS 2.  
 CC REPEAT 144 201 TNFR-CYS 3.  
 CC REPEAT 144 201 TNFR-CYS 4.  
 CC DOMAIN 306 365 DEATH DOMAIN.  
 CC DISULFID 41 54 BY SIMILARITY.  
 CC DISULFID 44 62 BY SIMILARITY.  
 CC DISULFID 65 80 BY SIMILARITY.  
 CC DISULFID 83 97 BY SIMILARITY.  
 CC DISULFID 87 105 BY SIMILARITY.  
 CC DISULFID 118 142 BY SIMILARITY.  
 CC DISULFID 145 160 BY SIMILARITY.  
 CC CARBOHYD 98  
 CC CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CONFLICT 263 263 A -> D (IN REF. 2 AND 3).  
 CC SEQUENCE 401 AA; 45996 MW; EB42FA51C9D7C71E CRC64;  
 Query Match 29.5%; Score 440.5; DB 4; Length 401;  
 Best Local Similarity 41.2%; Pred. No. 1.1e-31;  
 Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;  
 QY 5 PYPWDAETGERLVCAQCPPTGVORPCRRDSTTCGCPPHRYTQFWNYLERCVNV 64  
 DB 26 PKYLHYDEETSHOLLCKCPGPGTYLKQHTAKWKTCAPCPDHYTDSWHTSDECLYCS 85  
 QY 65 LCGEREEARACHATNRCACRTGFFAHAGFCLEHASCPGAGVIAPGTPSONTOCPC 124  
 DB 86 VKELQYVQECNTHNRVCEKEGYLEIEFCLKHRSCPPGPGVVOAGPERRNTVKRC 145  
 QY 125 PGTGTSASSSSSQCPHRNCTALGALNVPSSSHDTLCTCTGTFPLSTRVPGABE--C 182  
 DB 146 PDGFFSNSTSSAPCRKHTNCVSFGLLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202  
 QY 183 ERAVIDF 189  
 DB 203 EEAFFR 209

RESULT 4  
 O08727 ID O08727 PRELIMINARY; PRT; 401 AA.  
 AC O08727; DT 01-JUL-1997 (T-EMBLrel. 04, Created)  
 DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
 DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)  
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF).  
 GN TNFRSF11B OR OPG.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 ON NCBI\_Taxid=101116;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=INTESTINE;  
 RX MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,  
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 RA Suggs S., Boyle W.J.;  
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation  
 of bone density.";  
 RL Cell 89:309-319(1997).  
 CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
 CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY  
 CC SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC EMBL: U94330; AAB53707.1; -.  
 CC HSSP: P25942; ICDF.  
 CC InterPro: IPR000488; Death.  
 CC InterPro: IPR001368; TNFR\_c6.  
 CC Pfam: PF00020; TNFR\_c6; 4.  
 CC ProDom: PD000771; TNFR\_c6; 1.  
 CC SMART: SM00005; DEATH; 1.  
 CC SMART: SM00208; TNFR; 4.  
 CC PROSITE: PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 CC PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 CC Glycoprotein; Repeat; Cytokine; Signal.  
 CC SIGNAL 1 21 BY SIMILARITY.  
 CC CHAIN 22 401 OSTEOPROTEGERIN.  
 CC DOMAIN 23 201 4 X TNFR-CYS.  
 CC REPEAT 23 63  
 CC REPEAT 64 106 TNFR-CYS 1.  
 CC REPEAT 107 143 TNFR-CYS 2.  
 CC REPEAT 144 201 TNFR-CYS 3.  
 CC REPEAT 144 201 TNFR-CYS 4.  
 CC DOMAIN 306 365 DEATH DOMAIN.  
 CC DISULFID 41 54 BY SIMILARITY.  
 CC DISULFID 44 62 BY SIMILARITY.  
 CC DISULFID 65 80 BY SIMILARITY.  
 CC DISULFID 83 97 BY SIMILARITY.  
 CC DISULFID 87 105 BY SIMILARITY.  
 CC DISULFID 118 142 BY SIMILARITY.  
 CC DISULFID 145 160 BY SIMILARITY.  
 CC CARBOHYD 98  
 CC CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SEQUENCE 401 AA; 46192 MW; FEC6A31FD4E573A CRC64;  
 Query Match 28.5%; Score 425.5; DB 11; Length 401;  
 Best Local Similarity 39.5%; Pred. No. 2.5e-30;  
 Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;

QY 5 PTPWRDAETGERLVCAQCPPTGFVQPCRRDSTTCGCPGPPRHRYTQFWNYLRCRYCNV 64  
 Db 26 PKYLHYDPTGTHQLCDKCAPGYLYLKHOCIVRRKTLVCPGPDYSYDTSWHTSDCVYCS 85  
 QY 65 LCGEREEARACHATHNACRRTGFFAHAGFCLHASCPPGAGVIAPGTPSONTOCOPC 124  
 Db 86 VKELQTVQECNRTNVRVCEBEGRYLEFELCKHRSCPPGVLQAGTPERTNVCCKRC 145  
 QY 125 PPGTFSSASSSSQCPHNRCTALGLALNVPSSSHDTLCTCTGTFPLSTRVPCAE--C 182  
 Db 146 PDGFFSGTSSKAPCRKHTNCSLSGLLLIQGNATHDNV---CSGNREATQNGIDVTL 202  
 QY 183 ERAVIDFAFQDISIKRLQRLQAL 207  
 Db 203 EEAFFRFAVPTKIIPNWSLVLDL 227

RESULT 5  
 O08712 PRELIMINARY; PRT; 401 AA.  
 AC O08712; O70202;  
 DT 01-JUL-1997 (TREMblrel. 04, Created)  
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF).  
 DE TNRFSF11B OR OPG.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C; TISSUE-KIDNEY;  
 RX MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,  
 Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
 Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 Suggs S., Boyle W.J.;  
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation  
 of bone density.";  
 RT Cell 89:309-319(1997).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=129/OLA, AND NIH SWISS;  
 RC MEDLINE=98382527; PubMed=9714833;  
 RX Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,  
 Higashio K.;  
 RA "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)  
 gene and its expression in embryogenesis.";  
 RT Gene 215:339-343(1998).  
 RL CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
 OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
 SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
 OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
 STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,  
 BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND  
 PLACENTA. NOT DETECTED IN SPLEEN.  
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT  
 DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY  
 15 TO DAY 17.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; U94331; AAB53708.1; -;  
 DR EMBL; AB013898; BAA28269.1; -;  
 DR EMBL; AB013903; BAA33388.1; -;  
 DR EMBL; AB013899; BAA33388.1; JOINED.  
 DR EMBL; AB013900; BAA33388.1; JOINED.  
 DR EMBL; AB013901; BAA33388.1; JOINED.

DR EMBL; AB013902; BAA33388.1; JOINED.  
 DR HSSP; P25942; ICDF.  
 DR MGD; MGI:109587; Tnftrsf11b.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR ProDom; PD000771; TNFR\_c6; 1.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 KW Glycoprotein; Repeat; Cytokine; Signal.  
 FT SIGNAL 1 21 OSTEOPROTEGERIN.  
 FT CHAIN 22 401 4 X TNFR-CYS.  
 FT DOMAIN 23 201 TNFR-CYS 1.  
 FT REPEAT 23 63 TNFR-CYS 2.  
 FT REPEAT 64 106 TNFR-CYS 3.  
 FT REPEAT 107 143 TNFR-CYS 4.  
 FT REPEAT 144 201 DEATH DOMAIN.  
 FT DOMAIN 306 365 BY SIMILARITY.  
 FT DISULFID 41 54 BY SIMILARITY.  
 FT DISULFID 44 62 BY SIMILARITY.  
 FT DISULFID 65 80 BY SIMILARITY.  
 FT DISULFID 83 97 BY SIMILARITY.  
 FT DISULFID 87 105 BY SIMILARITY.  
 FT DISULFID 118 142 BY SIMILARITY.  
 FT DISULFID 145 160 BY SIMILARITY.  
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH  
 SWISS).  
 FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH  
 SWISS).  
 FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH  
 SWISS).  
 FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH  
 SWISS).  
 FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH  
 SWISS).  
 FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 28.5%; Score 424.5; DB 11; Length 401;  
 Best Local Similarity 39.0%; Pred. No. 3e-30;  
 Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;  
 QY 5 PTPWRDAETGERLVCAQCPPTGFVQPCRRDSTTCGCPGPPRHRYTQFWNYLRCRYCNV 64  
 Db 26 PKYLHYDPTGTHQLCDKCAPGYLYLKHOCIVRRKTLVCPGPDYSYDTSWHTSDCVYCS 85  
 QY 65 LCGEREEARACHATHNACRRTGFFAHAGFCLHASCPPGAGVIAPGTPSONTOCOPC 124  
 Db 86 VKELQTVQECNRTNVRVCEBEGRYLEFELCKHRSCPPGVLQAGTPERTNVCCKRC 145  
 QY 125 PPGTFSSASSSSQCPHNRCTALGLALNVPSSSHDTLCTCTGTFPLSTRVPCAE--C 182  
 Db 146 PDGFFSGTSSKAPCRKHTNCSLSGLLLIQGNATHDNV---CSGNREATQNGIDVTL 202  
 QY 183 ERAVIDFAFQDISIKRLQRLQAL 207  
 Db 203 EEAFFRFAVPTKIIPNWSLVLDL 227

RESULT 6  
 Q9PUS0 PRELIMINARY; PRT; 302 AA.  
 ID Q9PUS0  
 AC Q9PUS0  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)

DE DECOY RECEPTOR.  
OS Salvelinus fontinalis (Brook trout) (Brook char).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.  
ON NCBI\_TaxID=8038;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bobe J., Goetz F.W.;  
RT "A tumor necrosis factor receptor homolog is up-regulated in the brook trout (Salvelinus fontinalis) ovary at the completion of ovulation.";  
RL Biol. Reprod. 0:0-0(1999).  
DR EMBL: AF156738; AAD56428.1; -.  
DR HSSP: P19438; IEXT.  
DR InterPro: IPR000561; EGF-like.  
DR InterPro: IPR001368; TNFR\_c6.  
DR Pfam: PF00020; TNFR\_c6; 4.  
DR ProDom: PD000771; TNFR\_c6; 1.  
DR SMART: SM00208; TNFR; 4.  
DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 1.  
KW Receptor.  
SQ SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 26.5%; Score 395; DB 13; Length 302;  
Best Local Similarity 34.3%; Pred. No. 1e-27;  
Matches 82; Conservative 44; Mismatches 101; Indels 12; Gaps 7;  
QY 6 TYPWRDAETGERLVCAQCPGTFVORCRDPTTCGCPPRHYTQFWNYLERCRYCNVL 65  
DB 22 TFNDDRYSGLSIVCDRCPPGTLYRAPCSAMRKSDCACPNGAYTEFWNHISKLRCS-M 80  
QY 66 CGEREERARACHATHNRACRRTGFFAHAGF--CLEHASCPPGAGVIAPGTPSQNTQCP 123  
DB 81 CAENOVVKQECSPNSNCECEKGEYFNKYEACIKHKCPGPGVANTGTGPHQDTECVQ 140  
QY 124 CPPTGTSASSSEOCQPHRNCRTALGLALNVPSSSHDTLTCTSGTGPLSTRVPGAEECE 183  
DB 141 CQAGFSEVSATCATCQAQNSCKVGVVVLKGDWHNTLCASC--YDLKTR-DGAEYLH 197  
QY 184 RAVIDEV--AFODISIKRLQLQALEAPEGCGWPTPRAGRAALQLKRLRLTELLGAOD 240  
DB 198 EILPTFIQLHQTGIMKRRRL--AMRLPQGGKKPLIG--AVMKRNRRLHDFMNSWD 252

RESULT 7  
Q16042 PRELIMINARY; PRT; 425 AA.  
AC Q16042;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE TUMOR NECROSIS FACTOR RECEPTOR (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ON NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91370690; PubMed=1966549;  
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R., Brockhaus M., Lesslauer W.;  
RT "Two human TNF receptors have similar extracellular, but distinct intracellular, domain sequences.";  
RL Cytokine 2:231-237(1990).  
DR EMBL: S83368; AAB19824.2; -.  
DR HSSP: P25942; ICDF.  
DR InterPro: IPR001368; TNFR\_c6.  
DR Pfam: PF00020; TNFR\_c6; 4.  
DR ProDom: PD000771; TNFR\_c6; 1.  
DR SMART: SM00208; TNFR; 4.

DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
KW Receptor.  
FT NON\_TER 1  
SQ SEQUENCE 425 AA; 44608 MW; 1B24A97E3AD4CF9F CRC64;  
Query Match 22.7%; Score 338.5; DB 4; Length 425;  
Best Local Similarity 30.1%; Pred. No. 1.7e-22;  
Matches 82; Conservative 43; Mismatches 110; Indels 37; Gaps 9;  
QY 17 RLVCAQCPGTFVORCRDPTTCGCPPRHYTQFWNYLERCRYCNVLGGEREEARAC 76  
DB 15 QMCKSKSPGQAHKVFCTKTSDTVDCSDCEDSTYTQLMWNVPECLSCGSRCSDDQVETAC 74  
QY 77 HATHNRACRRTGFFAHAGF--FCLEHASCPPGAGVIAPGTPSQNTQCPGPGTFS 130  
DB 75 TREQNRICTCPGWYCALSKOEGCRLCAPLRKCRPGFVARPGTETSDVCKPCAPGTF 134  
QY 131 ASSSSSEOCQPHRNCRTALGLALNVPSSSHDTLTCTSGTGPLSTRVPGAEECERAVIDFV 190  
DB 135 NTSSTDICRPHQICNVVA---IPGNASMDAVCTSTS--PTRSMAPGAVHLPQV---- 184  
QY 191 AFODISIKRLQLQALEAPE---GWPPTPRA---GRAALQLKRLRLTELLGAODG 241  
DB 185 ---STRQHTQTPETPSTAPSTSLPMPGSPPAEGSTGDFALPVGLIVGTAL-----G 236  
QY 242 ALLVRLQLAL---RVARMP-GLERSVRERFLP 269  
DB 237 LLIGVNVVIMTQVKKKPLCLQREAKVPHLP 268

RESULT 8  
Q62327 PRELIMINARY; PRT; 459 AA.  
AC Q62327;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=NOD;  
RX MEDLINE=95178848; PubMed=7873884;  
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;  
RT "Allelic variation of the type 2 tumor necrosis factor receptor gene.";  
RL Mamm. Genome 5:726-727(1994).  
DR EMBL: X76401; CAA53981.1; -.  
DR HSSP: P19438; INCF.  
DR InterPro: IPR001368; TNFR\_c6.  
DR Pfam: PF00020; TNFR\_c6; 4.  
DR ProDom: PD000771; TNFR\_c6; 1.  
DR SMART: SM00208; TNFR; 4.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
FT NON\_TER 1  
FT VARIANT 87 87 S->T.  
FT VARIANT 93 93 T->I.  
FT VARIANT 268 268 F->I.  
FT VARIANT 345 345 S->F.  
FT VARIANT 421 421 Y->C.  
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 22.4%; Score 333.5; DB 11; Length 459;  
Best Local Similarity 29.7%; Pred. No. 5e-22;  
Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps 9;

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QY 17 RLVCAQCPGCTFVQPCRRDPTTCGCPPRHYTFQWNYLERCRYCNVLCGEREAEARAC 76
DB 37 QMCAKCPGGQYVYKHFCKNTSDTVACDEASMTQVNNQFRTCLSCSSCSTQDVETAC 96
QY 77 HATHNRACRGTGFF---AHAGF---CLEHASCPCGAGVIAPGTPSQNTQCPCPGTF 129
DB 97 TKQNRVCAACEAGRYCALKTHSGCRQMRSLKCGPGFGVASSRAPNGNVLKACAPGTF 156
QY 130 SASSSSEQCQPHRNCRTALGNVPGSSSHDTLCT---SCTGFPLSTRVPGAEECERA 185
DB 157 SDTSTSDVCRPHRCSILA---IFGNASTDAVCAPESTLSAIPRTLVSPQEPTRSQ 212
QY 186 VIDFVAPQDISIKRLQRLQALPAEGWGTPP-----RAGRAALQKLRLRTELGAQD 240
DB 213 PLD-----QEPGSPQTSILTSL-----GSTPIIEQSTKGGISLPIGLIVGVTSL----- 257
QY 241 GALLVRLQLAL-----RVARMPLGLSRYRERFLP 269
DB 258 GLLMLGLVNCFILVQRKKPKSCLQORDAKVPHVP 290

RESULT 9
O88734 PRELIMINARY; PRT; 482 AA.
AC O88734;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
BT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE P80 TNF-ALPHA RECEPTOR.
GN TNFR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hurler B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT "The Mouse Tumor Necrosis Factor Receptor Gene: Genomic Structure and
RT Characterization of the two Transcripts.";
RL Genomics 0:0-0(0).
DR EMBL; Y14619; CAA74969.1;
DR EMBL; Y14620; CAA74969.1; JOINED.
DR EMBL; Y14621; CAA74969.1; JOINED.
DR EMBL; Y14622; CAA74969.1; JOINED.
DR EMBL; Y14623; CAA74969.1; JOINED.
DR EMBL; Y14624; CAA74969.1; JOINED.
DR HSSP; P19438; INCF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FFB3C CRC64;

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Query Match 21.9%; Score 327; DB 11; Length 482;
Best Local Similarity 29.3%; Pred. No. 2e-21;
Matches 82; Conservative 43; Mismatches 109; Indels 46; Gaps 10;

QY 17 RLVCAQCPGCTFVQPCRR---DSPTTCGCPPRHYTFQWNYLERCRYCNVLCGER 69
DB 52 QMCAKCPGGQYVYKHFCKNTSDTVACADSDTVACDEASMTQVNNQFRTCLSCSSCSTD 111
QY 70 EEARACHATHNRACRGTGFF---AHAGF---CLEHASCPCGAGVIAPGTPSQNTQCQ 122
DB 112 QVETRACRKOONRVCAACEAGRYCALKTHSGCRQMRSLKCGPGFGVASSRAPNGNVLK 171
QY 123 PCPPGTFSSASSSSSEQCQPHRNCRTALGNVPGSSSHDTLCT---SCTGFPLSTRVPG 178
DB 172 ACAPGTFSDTSTSDVCRPHRCSILA---IPGNASTDAVCAPESTLSAIPRTLVVSQ 227
QY 179 AEECERAVIDFVAFQDISIKRLQRLQALPAEGWGTPP-----RAGRAALQKLRLRLT 233

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DB 228 PEPTRSQPLD-----QEPGSPQTSILTSL-----GSTPIIEQSTKGGISLPIGLIVGT 277
QY 234 ELLGAQOGALLVRLQLAL-----RVARMPLGLSRYRERFLP 269
DB 278 SL-----GLLMLGLVNCFILVQRKKPKSCLQORDAKVPHVP 312

RESULT 10
Q98SM6 PRELIMINARY; PRT; 630 AA.
AC Q98SM6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DEATH RECEPTOR 6 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "Expression of DR6 in the ovary.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349908; AAK29666.1;
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 630 AA; 68977 MW; 53C53BD1C4B25567 CRC64;

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Query Match 19.9%; Score 297; DB 13; Length 630;
Best Local Similarity 34.2%; Pred. No. 1.3e-18;
Matches 55; Conservative 27; Mismatches 79; Indels 0; Gaps 0;

QY 11 DAETGERLVCAQCPGPTFVQPCRRDPTTCGCPPRHYTFQWNYLERCRYCNVLCGERE 70
DB 22 DRATNELICDKCPAGTVVSKHCTKSLRECSPCPDGTFTHKENGIERCHPCRPCELPM 81
QY 71 EEARACHATHNRACRGTGFFAHAGFLEHASCPCGAGVIAPGTPSQNTQCPCPGTFSS 130
DB 82 IEKTHCTALTDRCTCLSGTFQINDTCVPTVCPGVGVRKKGTETEDVRCKPCPGTFSS 141
QY 131 ASSSSSEQCQPHRNCRTALGNVPGSSSHDTLCTSGTGP 171
DB 142 DVPSSVMKCKTYTDCFGKNVYVYKPKESDNVCGSPASLP 182

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RESULT 11
Q98PU5 PRELIMINARY; PRT; 655 AA.
AC Q98PU5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=KIDNEY;
RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA Minami M.;
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
RT (DR6).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF322069; AAG38115.1;
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 10, 2002, 10:59:24 ; Search time 15.03 Seconds  
(without alignments)  
661.089 Million cell updates/sec

Title: US-09-280-567-6  
Perfect score: 1491  
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVAMPGLERSVRERFLPVH 271

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	342.5	23.0	461	1	TNR2_HUMAN
2	332.5	22.3	474	1	TNR2_MOUSE
3	299.5	20.1	435	1	TNR2_HUMAN
4	265.5	17.8	415	1	TNR2_MOUSE
5	260	17.4	349	1	VC22_VARV
6	244	16.4	283	1	TR14_HUMAN
7	234.5	15.7	325	1	VT2_SFVKA
8	215.5	14.5	277	1	OX40_HUMAN
9	211.5	14.2	271	1	OX40_RAT
10	211	14.2	277	1	CD40_HUMAN
11	210.5	14.1	326	1	VT2_MTXVL
12	203	13.6	289	1	CD40_MOUSE
13	202	13.5	269	1	CD40_BOVIN
14	194.5	13.0	272	1	OX40_MOUSE
15	185	12.4	256	1	41BB_MOUSE
16	182	12.2	595	1	CD30_HUMAN
17	174	11.7	255	1	41BB_HUMAN
18	171.5	11.5	416	1	NGFR_CHICK
19	168	11.3	425	1	NGFR_RAT
20	163	10.9	332	1	FASA_PIG
21	158	10.6	427	1	NGFR_HUMAN
22	155.5	10.4	327	1	FASA_MOUSE
23	155	10.4	323	1	FASA_BOVIN
24	153	10.3	241	1	TR18_HUMAN
25	148	9.9	250	1	CD27_MOUSE
26	147.5	9.9	5376	1	ZAN_MOUSE
27	145	9.7	335	1	FASA_HUMAN
28	143.5	9.6	471	1	TNR1_BOVIN
29	142.5	9.6	260	1	CD27_HUMAN
30	137.5	9.2	324	1	FASA_RAT
31	130.5	8.8	454	1	TNR1_MOUSE
32	128.5	8.6	417	1	WSL1_HUMAN
33	128.5	8.6	3635	1	LMA5_MOUSE

34	127	8.5	1192	1	LMG2_MOUSE	Q61092	mus musculus
35	125.5	8.4	1877	1	PKC5_MOUSE	Q04592	mus musculus
36	124.5	8.4	1696	1	PKC5_BRACL	Q9nj15	branchiostoma
37	124.5	8.4	1713	1	LMA3_HUMAN	P16787	homo sapien
38	123.5	8.3	455	1	TNR1_HUMAN	P19438	homo sapien
39	123	8.2	2569	1	LMA3_MOUSE	Q61789	mus musculus
40	121	8.1	3106	1	LMG2_MOUSE	Q60675	mus musculus
41	120	8.0	1609	1	LMG1_HUMAN	P11047	homo sapien
42	119.5	8.0	3084	1	LMG1_MOUSE	P19137	mus musculus
43	118.5	7.9	461	1	TNR1_RAT	P22934	rattus norv
44	118.5	7.9	1680	1	FUR2_DROME	P30432	drosophila
45	118	7.9	913	1	PKC5_HUMAN	Q92824	homo sapien

## ALIGNMENTS

RESULT 1	
TNR2_HUMAN	
ID TNR2_HUMAN STANDARD; PRT; 461 AA.	
AC P20333;	
DT 01-FEB-1991 (Rel. 17, Created)	
DT 01-AUG-1991 (Rel. 19, Last sequence update)	
DT 20-AUG-2001 (Rel. 40, Last annotation update)	
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR	
DE BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT).	
GN TNFRSF1B OR TNFR2 OR TNFR.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=90260639; PubMed=2160731;	
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,	
RA Dower S.K., Cosman D., Goodwin R.G.;	
RT "A receptor for tumor necrosis factor defines an unusual family of	
RT cellular and viral proteins.";	
RL Science 248:1019-1023(1990).	
RN [2]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=91045991; PubMed=2172983;	
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,	
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;	
RT "A second tumor necrosis factor receptor gene product can shed a	
RT naturally occurring tumor necrosis factor inhibitor.";	
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).	
RN [3]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=96299745; PubMed=8661109;	
RA Beltlinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,	
RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,	
RA Brodeur G.M.;	
RT "Physical mapping and genomic structure of the human TNFR2 gene.";	
RL Genomics 35:94-100(1996).	
RN [4]	
RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.	
RX MEDLINE=90349572; PubMed=2166946;	
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,	
RA Ringold G.M.;	
RT "Complementary DNA cloning of a receptor for tumor necrosis factor	
RT and demonstration of a shed form of the receptor.";	
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).	
RN [5]	
RP SEQUENCE OF 27-31.	
RX MEDLINE=90110215; PubMed=2153136;	
RA Engelmann H., Novick D., Wallach D.;	
RT "Two tumor necrosis factor-binding proteins purified from human	
RT urine. Evidence for immunological cross-reactivity with cell surface	
RT tumor necrosis factor receptors.";	
RL J. Biol. Chem. 265:1531-1536(1990).	
RN [6]	
RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.	



RT necrosis factor receptors demonstrate one receptor is species  
 RT specific.", Acad. Sci. U.S.A. 88:2830-2834(1991).  
 RL [2]

RN SEQUENCE FROM N.A.  
 RX MEDLINE=91246168; PubMed=1645445;  
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,  
 RA Copeland N.G., Jenkins N.A., Smith C.A.;  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 RT receptors for tumor necrosis factor,"  
 RL Mol. Cell. Biol. 11:3020-3026(1991).  
 RN [3]

RN SEQUENCE OF 1-26 FROM N.A.

RC STRAIN=NOD;  
 RA Jacob C.O., Liu J.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]

RC SEQUENCE OF 1-22 FROM N.A.

RA Kisonerghis M., Fellows R., Feldmann M., Chernajovsky Y.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----

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 CC -----

DR EMBL; M60469; AAA39752.1; -

DR EMBL; M59378; AAA40463.1; -

DR EMBL; U39488; AAA85021.1; -

DR EMBL; X87128; CAA60618.1; -

DR PIR; B38634; B38634.

DR HSP; P19438; INCF.

DR MGD; MGI:1314883; Tnfrsf1b.

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00020; TNFR\_c6; 4.

DR ProDom; PD000771; TNFR\_c6; 1.

DR SMART; SM00208; TNFR; 4

DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.

FW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 22

FT CHAIN 23 474

FT DOMAIN 23 258

FT TRANSMEM 259 288

FT DOMAIN 289 474

FT DOMAIN 39 203

FT REPEAT 39 77

FT REPEAT 78 119

FT REPEAT 120 164

FT REPEAT 165 203

FT DISULFID 40 54

FT DISULFID 55 68

FT DISULFID 58 76

FT DISULFID 79 94

FT DISULFID 97 111

FT DISULFID 101 119

FT DISULFID 121 127

FT DISULFID 136 145

FT DISULFID 139 163

FT DISULFID 166 181

FT CARBOHYD 69 69

FT CARBOHYD 195 195

SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Best Local Similarity 29.7%; Pred. No. 2 le-19;  
 Matches 81; Conservative 44; Mismatches 109; Indels 39; Gaps 9;

QY 17 RLVCACQPGTFTVQRCRRDSPTTCGPPRHYTQFWNYLRCRYCNVLCGEREEARAC 76  
 : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : |||||

Db 52 QMCCAKCPGQVVKHFCNKTSITVDCADCEASMYTQVWQNFRTCLSCSSCTTQDVEIRAC 111  
 : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : |||||

QY 77 HATHNACRCRTGFF-----AHAGF---CLEHASCPPGAGVIAGTPTSONTCQCPGTF 129  
 : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : |||||

Db 112 TKQNRVCAACEAGRYCALKTHSGCRQRLSKGPGFVASSRANGNVLCACAPGF 171  
 : : ||||| : : : : ||||| : : : : ||||| : : : : ||||| : : : : |||||

QY 130 SASSSSEOCPHRNCTALGLANVPSSSHDTLCT-----SCTGFPLSTRVPGAECCERA 185  
 : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : |||||

Db 172 SDTSTSDVCRPHRICSLA----IFGNASTDAVCAPESTLSAIPRTLYVSQPEPTRSQ 227  
 : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : |||||

QY 186 VIDFAVQDISIKRLQRLQALAEPEGWPTP-----RAGRAALQKLRRRLTELGLAQD 240  
 : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : |||||

Db 228 PLD-----QEPGPSQTSILTSL-----GSTPIEQSTKGGISLIGLVGVTSL----- 272  
 : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : |||||

QY 241 GALLVRLQAL---RVARMPLGLSVRERFLP 269  
 : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : |||||

Db 273 GLLMGLVNCIILVQRKKRPSCLQRDAKVPHVP 305  
 : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : ||||| : : |||||

RESULT 3  
 TNRC\_HUMAN STANDARD; PRT; 435 AA.

ID TNRC\_HUMAN STANDARD; PRT; 435 AA.

AC P36941;  
 DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR  
 DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).

GN LTBR OR TNFR OR TNFRSF3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;  
 RX MEDLINE=93252381; PubMed=8486360;

RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;  
 RT "Construction and evaluation of a hncDNA library of human 12p

RL transcribed sequences derived from a somatic cell hybrid.";  
 RN Genomics 16:214-218(1993).

RP FUNCTION.  
 RX MEDLINE=94225209; PubMed=8171323;

RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,  
 RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;

RT "A lymphotoxin-beta-specific receptor.";  
 RL Science 264:707-710(1994).

CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
 CC IMMUNE DEVELOPMENT.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

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 CC -----

CC EMBL; L04270; AAA36757.1; -

DR HSP; P25942; ICDF.

DR MIM; 600979; -

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00020; TNFR\_c6; 4.

DR ProDom; PD000771; TNFR\_c6; 1.

DR SMART; SM00208; TNFR; 4.

Query Match 22.3%; Score 332.5; DB 1; Length 474;



ID TR14\_HUMAN STANDARD; PRT; 283 AA.  
 AC Q92956; Q90M65;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 14 PRECURSOR  
 DE (HERPESVIRUS ENTRY MEDIATOR) (TUMOR NECROSIS FACTOR RECEPTOR-LIKE 2)  
 DE (TR2).  
 GN TNFRSF14 OR HVEM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cervix adenocarcinoma;  
 RC MEDLINE=97053782; PubMed=8898196;  
 RX Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;  
 RA "Herpes simplex virus-1 entry into cells mediated by a novel member of  
 RT the TNF/NGF receptor family.";  
 RL Cell 87:427-436(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=97306336; PubMed=9162061;  
 RX Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,  
 RA Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,  
 RA Porter T.G., Truneh A., Young P.R.;  
 RA "A newly identified member of the tumor necrosis factor receptor  
 RT superfamily with a wide tissue distribution and involvement in  
 RT lymphocyte activation.";  
 RL J. Biol. Chem. 272:14272-14276(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Zhang W., Wan T., Cao X.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -! FUNCTION: RECEPTOR FOR TNFRSF14. INVOLVED IN LYMPHOCYTE ACTIVATION.  
 CC PLAYS AN IMPORTANT ROLE IN HSV PATHOGENESIS BECAUSE IT ENHANCED  
 CC THE ENTRY OF SEVERAL WILDTYPE HSV STRAINS OF BOTH SEROTYPES INTO  
 CC CHO CELLS, AND MEDIATED HSV ENTRY INTO ACTIVATED HUMAN T CELLS.  
 CC -! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABLE).  
 CC -! TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION  
 CC IN LUNG, SPLEEN, AND THYMUS.  
 CC -! SIMILARITY: CONTAINS 1 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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CC  
EMBL; U70321; AAB58354.1; -  
EMBL; U81232; AAD00505.1; -  
DR EMBL; AF153978; AAF75588.1; -  
DR HSSP; P25942; 1CDF.  
DR MIM; 602746; -  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF000020; TNFR\_c6; 3.  
DR ProDom; PD000771; TNFR\_c6; 1.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 38 POTENTIAL.  
FT CHAIN 39 283 TUMOR NECROSIS FACTOR RECEPTOR  
FT FT SUPERFAMILY MEMBER 14.  
FT DOMAIN 39 202 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 203 223 POTENTIAL.

FT DOMAIN 224 283  
 FT CYTOPLASMIC (POTENTIAL).  
 FT 3 X TNFR-CYS.  
 FT REPEAT 42 162  
 FT TNFR-CYS 1.  
 FT REPEAT 42 75  
 FT TNFR-CYS 2.  
 FT REPEAT 121 119  
 FT TNFR-CYS 3.  
 FT DISULFID 42 53  
 FT BY SIMILARITY.  
 FT DISULFID 54 67  
 FT BY SIMILARITY.  
 FT DISULFID 57 75  
 FT BY SIMILARITY.  
 FT DISULFID 78 93  
 FT BY SIMILARITY.  
 FT DISULFID 96 111  
 FT BY SIMILARITY.  
 FT DISULFID 99 119  
 FT BY SIMILARITY.  
 FT DISULFID 121 127  
 FT BY SIMILARITY.  
 FT DISULFID 138 162  
 FT BY SIMILARITY.  
 FT CARBOHYD 110 110  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 173 173  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 17 17  
 FT K > R (IN REF. 1).  
 SQ SEQUENCE 283 AA; 30392 MW; 46CE13C2C70242C1 CRC64;

Query Match 16.4%; Score 244; DB 1; Length 283;  
 Best Local Similarity 37.3%; Pred. No. 1.3e-12;  
 Matches 56; Conservative 14; Mismatches 68; Indels 12; Gaps 4;

QY 20 CAQCPGCTFVORPCRRDPTTCGCPRHRYTQFWNYLER---CRYCNVLCGEREEARAC 76  
 Db 54 CPKCSGPGYRKEACGELTGTVCPEPGTYIAHLNGLSKLCQCMCDPAMGLR--ASRNC 111  
 QY 77 HATHNRACRCRTGFFA-----HAGFCLHACGPPGAGVIAPGTPSNTQCQPCPGCTFS 130  
 Db 112 SRTEAVCGCGSPGHFCIVQGDHCACRAYATSSPGORVOKGTESQDTLCQNCPPGTF 171  
 QY 131 ASSSSSQCPQHRNCTALGLALNVPSSSH 160  
 Db 172 -PNTLEECQHOTKCSLWTKAGAGTSSSH 200

RESULT 7  
 VT2\_SFVKA  
 ID VT2\_SFVKA STANDARD; PRT; 325 AA.  
 AC P25943;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).  
 GN T2.  
 OS Shope fibroma virus (strain Kasza) (SFV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Leporipoxvirus.  
 OX NCBI\_TaxID=10272;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87321103; PubMed=2820128;  
 RA Upton C., Delange A.M., McFadden G.;  
 RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the  
 RT telomeric region of the Shope fibroma virus genome.";  
 RL Virology 160:20-30(1987).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=91207415; PubMed=1850261;  
 RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrar T., Upton C.,  
 RA McFadden G., Goodwin R.G.;  
 RT "T2 open reading frame from the Shope fibroma virus encodes a soluble  
 RT form of the TNF receptor.";  
 RL Biochem. Biophys. Res. Commun. 176:335-342(1991).  
 CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO  
 CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL  
 CC ANTIVIRAL EFFECTS OF THE CYTOKINE.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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 CC -----  
 CC EMBL; M17433; ; NOT\_ANNOTATED\_CDS.  
 DR EMBL; A23727; CAA01687.1; -.  
 DR PIR; B43692; B43692.  
 DR HSSP; P19438; 1TNR.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 2.  
 DR ProDom; PD000771; TNFR\_c6; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00500; TNFR\_NGFR\_2; 1.  
 KW Receptor; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 16 POTENTIAL.  
 FT CHAIN 17 325 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.  
 FT DOMAIN 27 186 4 X TNFR-CYS.  
 FT REPEAT 27 62 TNFR-CYS 1.  
 FT REPEAT 63 104 TNFR-CYS 2.  
 FT REPEAT 105 147 TNFR-CYS 3.  
 FT REPEAT 148 186 TNFR-CYS 4.  
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;

Query Match 15.7%; Score 234.5; DB 1; Length 325;  
 Best Local Similarity 32.9%; Pred. No. 8.3e-12;  
 Matches 52; Conservative 19; Mismatches 76; Indels 11; Gaps 3;

QY 18 LVCAQCPGCTFVORPCRRDPTTCGCPRHRYTQFWNYLERCRYCNVLCGEREEARACH 77  
 Db 38 LCCASCHPGFYASRLCGPSNTVCSPCEDGTFSTNHPACVSCRGPCPTHLSSESQPCD 97  
 QY 78 ATHNRACRCRTGFFA-----HAGFCLHACGPPGAGVIAPGTPSNTQCQPCPGTFSA 131  
 Db 98 RTHDRVNCSTGNYVCLLKQNGCRICAPQTKCPAGYGV-SGHTRAGDTLCKCPHPTYS 156  
 QY 132 SSSSSQCPQHRNCTALGLALNVPSSSHDTLCTCTG 169  
 Db 157 SLSPTERCSTGFNYISVGFNL----YFVNETSCTTTAG 190

RESULT 8  
 OX40\_HUMAN  
 ID OX40\_HUMAN STANDARD; PRT; 277 AA.  
 AC P43489; Q13663;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY  
 DE ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).  
 GN TNFRSF4 OR TXGPI.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94170844; PubMed=7510240;  
 RA Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F.,  
 RA Hummel M., Fonatsch C., Stein H.;  
 RT "The human OX40 homolog: cDNA structure, expression and chromosomal  
 RT assignment of the ACT35 antigen.";  
 RL Eur. J. Immunol. 24:677-683(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95219871; PubMed=7704935;  
 RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,  
 RA Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;

"Identification of OX40 ligand and preliminary characterization of its activities on OX40 receptor.";

RL CIRC. Shock 44:30-34(1994).

CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;

CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd134.htm".

CC -----

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CC -----

DR EMBL; X75962; CAA53576.1; .

DR EMBL; S76792; AAB33944.1; ALT\_INIT.

DR HSSP; P25942; ICDF.

DR MIM; 600315; .

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00020; TNFR\_c6; 3.

DR ProDom; PD000771; TNFR\_c6; 1.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.

DR Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;

KW Signal.

FT SIGNAL 1 28 POTENTIAL.

FT CHAIN 29 277 OX40L RECEPTOR.

FT DOMAIN 29 214 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 215 235 POTENTIAL.

FT DOMAIN 236 277 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 30 169 4 X TNFR-CYS.

FT REPEAT 30 65 TNFR-CYS 1.

FT REPEAT 66 107 TNFR-CYS 2.

FT REPEAT 108 126 TNFR-CYS 3 (INCOMPLETE).

FT REPEAT 127 167 TNFR-CYS 4.

FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;

Query Match 14.5%; Score 215.5; DB 1; Length 277;

Best Local Similarity 27.0%; Pred. No. 2.3e-10;

Matches 72; Conservative 22; Mismatches 104; Indels 69; Gaps 11;

QY 6 TYPWRDAETGERLVCAOCPPGCTFVQRCRDSPTTCGCPPRHYTQFNNY--LERCRCYN 63

DB 35 TYPNSDR-----CCHCECRGNGMVSRCSQNTVCRPGGFGFNDVYSSKPKPCPTWCN 88

QY 64 VLCCEREERARACHATHNRACRGTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCOP 123

DB 89 LRSG--SERKQLCTATQDTCRCRAG-----TQPLDSYKPG-----VDCAP 127

QY 124 CPPTFFSASSSSSQOPHNRCTALGALNVPGSSSHDTLCTS---CTGFLPLSTRVPGAE 180

DB 128 CPPGHF--SPGDNOACKPWTNCTLAGKHTLQPASNSDAICEDRDPPATQPTQGGPAR 185

QY 181 ECERAVIDFAVFQDISIKRLQRLQALAEPEGW-----GPTPR-----AGRAALQLKLRR 230

DB 186 PI-----TVQTEAMPRTSQGSPSTRVPEVPGGRAVAAILGLG 222

QY 231 RLTELLAQDQGALIVRLQLALRVAMP 257

DB 223 LVGLGLGL--AIIALLYLRLRDLRP 247

RESULT 9

OX40\_RAT

ID OX40\_RAT

AC P15725;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).

GN TNFRSF4 OR TXGP1L OR OX40.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=T-cell;

RX MEDLINE=90214614; PubMed=2157591;

RA Mallett S., Fossum S., Barclay A.N.;

RT "Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.";

RL EMBO J. 9:1063-1068(1990).

CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC -----

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CC -----

DR EMBL; X17037; CAA34897.1; .

DR PIR; S08036; S08036.

DR PIR; S12783; S12783.

DR HSSP; P25942; ICDF.

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00020; TNFR\_c6; 3.

DR ProDom; PD000771; TNFR\_c6; 1.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.

DR Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;

KW Signal.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 271 OX40L RECEPTOR.

FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 211 235 POTENTIAL.

FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 25 164 4 X TNFR-CYS.

FT REPEAT 25 60 TNFR-CYS 1.

FT REPEAT 61 102 TNFR-CYS 2.

FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).

FT REPEAT 124 164 TNFR-CYS 4.

FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 14.2%; Score 211.5; DB 1; Length 271;

Best Local Similarity 31.5%; Pred. No. 4.6e-10;

Matches 53; Conservative 18; Mismatches 54; Indels 43; Gaps 8;

QY 6 TYPWRDAETGERLVCAOCPPGCTFVQRCRDSPTTCGCPPRHYTQFNNY--LERCRCYN 63

DB 30 TYP-----SGHK--CCRCQPGHGMVSRCDHTDVTCHPCPEFGFYNEAVNYDTCQCTQCN 83

QY 64 VLCCEREERARACHATHNRACRGTGFFAHAGFCLEHASCPPGAGVIAPGT--PSQNT--- 119

DB 84 HRSG--SELKQNTPTEDTVCQCR-----PGTQPRQDSSHK 117

QY 120 ---QCQCPPEPTFSASSSSSQOPHNRCTALGALNVPGSSSHDTLCL 164

DB 118 LGVDCVCPGPHF--SPGSNQACKPWTNCTLSGKQIRHPASNSLDTVC 163

```
RESULT 10
CD40_HUMAN          STANDARD;          PRT;    277 AA.
ID   CD40_HUMAN
AC   P25942;
DT   01-MAY-1992 (Rel. 22, Created)
DI   01-MAY-1992 (Rel. 22, Last sequence update)
DE   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40)
DE   (TUMOR NECROSIS FACTOR RECEPTOR 5).
GN   TNFRSF5 OR CD40.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89356608; PubMed=2475341;
RA   Stamenkovic I., Clark E.A., Seed B.;
RT   "A B-lymphocyte activation molecule related to the nerve growth
RT   factor receptor and induced by cytokines in carcinomas.";
RL   EMBO J. 8:1403-1410(1989).
RN   [2]
RP   3D-STRUCTURE MODELING OF 24-144.
RX   MEDLINE=97189482; PubMed=9037712;
RA   Bajorath J., Aruffo A.;
RT   "Construction and analysis of a detailed three-dimensional model of
RT   the ligand binding domain of the human B cell receptor CD40.";
RL   Proteins 27:59-70(1997).
RN   [3]
RP   3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX   MEDLINE=98286533; PubMed=9605317;
RA   Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RA   Zheng Z., Naismith J.H., Thomas D.;
RT   "The role of polar interactions in the molecular recognition of CD40L
RT   with its receptor CD40.";
RL   Protein Sci. 7:1124-1135(1998).
CC   -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC   -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC   -1- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -1- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
CC   WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
CC   -----
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; X60592; CAA43045.1; -
DR   PIR; S04460; S04460.
DR   PDB; ICDF; 01-APR-97.
DR   MIM; 109535; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS00050; TNFR_NGFR_2; 4.
KW   Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
KW   3D-structure.
FT   SIGNAL          1 19      POTENTIAL.
FT   CHAIN          20 277    CD40L RECEPTOR.
FT   DOMAIN         20 193    EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      194 215    POTENTIAL.
FT   DOMAIN         216 277    CYTOPLASMIC (POTENTIAL).
FT   DOMAIN         25 187    4 X TNFR-CYS.
FT   REPEAT         25 60     TNFR-CYS 1.
FT   REPEAT         61 103    TNFR-CYS 2.
FT   REPEAT        104 144    TNFR-CYS 3.
FT   REPEAT        145 187    TNFR-CYS 4.
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FT   DISULFID       26 37     FT
FT   DISULFID       38 51     FT
FT   DISULFID       41 59     FT
FT   DISULFID       62 77     FT
FT   DISULFID       83 103    FT
FT   DISULFID      105 119    FT
FT   DISULFID      111 116    FT
FT   DISULFID      125 143    FT
FT   CARBOHYD       153 153    FT
FT   CARBOHYD       180 180    FT
SQ   SEQUENCE       277 AA; 30619 MW; BC8776EC2C4A5680 CRC64;
      Query Match      14.2%; Score 211; DB 1; Length 277;
      Best Local Similarity 30.5%; Pred. No. 5 le-10;
      Matches 46; Conservative 21; Mismatches 76; Indels 8; Gaps 3;
OY   20 CAOCPPGTFTVORPCRRDSTTCGCPRRHYTFQWNYLERC---RYCNVLCGEREEARAC 76
      A B-lymphocyte activation molecule related to the nerve growth
DB   38 CSLCQPGOKLVSDCTETETETCLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGT 97
      factor receptor and induced by cytokines in carcinomas.";
OY   77 HATHNRACRRTGFFAHA---GFCLEHASGPPGAGVIAPGTPSONTOCQPCPGTFSASS 133
      "A B-lymphocyte activation molecule related to the nerve growth
DB   98 ET--DTTICTCEGWHCTSEACSCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVS 155
      factor receptor and induced by cytokines in carcinomas.";
OY   134 SSSEOCQPHRNCTALGIALNVPGSSSHDTLC 164
      "The role of polar interactions in the molecular recognition of CD40L
DB   156 SAFEKCHPWTSCTEKDLVVOQAGTKNTDVC 186
      with its receptor CD40.";
RESULT 11
VT2_MXVXL
ID   VT2_MXVXL      STANDARD;          PRT;    326 AA.
AC   P29825;
DT   01-APR-1993 (Rel. 25, Created)
DI   01-APR-1993 (Rel. 25, Last sequence update)
DI   15-JUL-1999 (Rel. 38, Last annotation update)
DE   TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN   T2.
OS   Myxoma virus (strain Lausanne).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Leporipoxvirus.
OC   NCBI_TaxID=31530;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91335768; PubMed=1651597;
RA   Upton C., Macen J.L., Schreiber M., McPadden G.;
RT   "Myxoma virus expresses a secreted protein with homology to the tumor
RT   necrosis factor receptor gene family that contributes to viral
RT   virulence.";
RL   Virology 184:370-382(1991).
CC   -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC   REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC   ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC   -1- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -----
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; M95181; AAA46632.1; -.
DR   EMBL; A23729; CAA01688.1; -.
DR   PIR; A40566; GQVZML.
DR   HSSP; P19438; ITNR.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
```



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DR PROSITE: PS00050: TNFR_NGFR_2; 2.  
KW Receptor; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 16 POTENTIAL.  
FT CHAIN 17 326 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.  
FT DOMAIN 27 186 4 X TNFR-CYS.  
FT REPEAT 27 62 TNFR-CYS 1.  
FT REPEAT 63 104 TNFR-CYS 2.  
FT REPEAT 105 147 TNFR-CYS 3.  
FT REPEAT 148 186 TNFR-CYS 4.  
FT CARBOHYD 66 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 181 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 326 AA: 35208 MW: ABBF027E947292FF CRC64;  
  
Query Match 14.1%; Score 210.5; DB 1; Length 326;  
Best Local Similarity 30.4%; Pred. No. 6.6e-10;  
Matches 48; Conservative 19; Mismatches 80; Indels 11; Gaps 3;  
  
QY 18 LVCAQCPGTFVQRCRDSPTTCGCPRRHYTFQWNYLERCYNVLGGEREEARACH 77  
DB 38 LCCTSCPGSYASRLCGPGSDTVCSPCKNETFTASTNHAPACVSCRGRCCTGHLSESQSCD 97  
  
QY 78 ATHNRACRRTGFFA-----HAGFCLHASCPPGAGVIAPGTPSONTOCQCPPTGESA 131  
DB 98 KTRDRVCDSCAGNYCLLKQEGCRICAPTKCPAGIGV-SGHTRTGDLVLTCKPRITYSD 156  
  
QY 132 SSSSSQCPHRRNCTALGLALNVPGSSSHDTLCTCTG 169  
DB 157 AVSSTCTSSFNVISVEFNL-----YVNDTSCITTAG 190  
  
RESULT 12  
CD40_MOUSE  
ID CD40_MOUSE STANDARD; PRT; 289 AA.  
AC P27512;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).  
GN TNFRSF5 OR CD40.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92105763; PubMed=1370315;  
RA Torres R.M.; Clark E.A.;  
RT "Differential increase of an alternatively polyadenylated mRNA  
species of murine CD40 upon B lymphocyte activation."  
RL J. Immunol. 148:620-626(1992).  
RN [2]  
RP REVISIONS.  
RC STRAIN=BALB/C;  
RA Torres R.M.;  
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C; TISSUE=Liver;  
RX MEDLINE=93094586; PubMed=1281194;  
RA Grimaldi J.C.; Torres R.; Kozak C.A.; Chang R.; Clark E.A.;  
RA Howard M.; Cockayne D.A.;  
RT "Genomic structure and chromosomal mapping of the murine CD40 gene."  
RL J. Immunol. 149:3921-3926(1992).  
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC  
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CC -----  
DR EMBL: M83312; AAB08705.1; -  
DR EMBL: M94126; AAA37404.1; -  
DR EMBL: M94129; AAA37404.1; JOINED.  
DR EMBL: M94128; AAA37404.1; JOINED.  
DR EMBL: M94127; AAA37404.1; JOINED.  
DR PIR: A46476; A46476.  
DR HSSP: P25942; 1CDF.  
DR MGD: MGI:88336; Tnfrsf5.  
DR InterPro: IPR001388; TNFR_c6.  
DR Pfam: PF00020; TNFR_c6; 4.  
DR ProDom: PD000771; TNFR_c6; 1.  
DR SMART: SM00208; TNFR; 4.  
DR PROSITE: PS00652; TNFR_NGFR_1; 1.  
DR PROSITE: PS00050; TNFR_NGFR_2; 4.  
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 289 CD40L RECEPTOR.  
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 194 215 POTENTIAL.  
FT DOMAIN 216 289 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 25 187 4 X TNFR-CYS.  
FT REPEAT 25 60 TNFR-CYS 1.  
FT REPEAT 61 103 TNFR-CYS 2.  
FT REPEAT 104 144 TNFR-CYS 3.  
FT REPEAT 145 187 TNFR-CYS 4.  
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 289 AA: 32111 MW: C791CB6D2FEA574E CRC64;  
  
Query Match 13.6%; Score 203; DB 1; Length 289;  
Best Local Similarity 31.1%; Pred. No. 2.3e-09;  
Matches 47; Conservative 19; Mismatches 77; Indels 8; Gaps 3;  
  
QY 20 CAOCPPGTFVQRCRDSPTTCGCPRRHYTFQWNYLERC---RYCNVLGGEREEARAC 76  
DB 38 CDLCQPGSLTSTALEKTQCHPCDSGEFSAQWNRIRCHQHRHCEPNOGLRVKKEGT- 96  
  
QY 77 HATHNRACRRTGFFA---HAGFCLHASCPPGAGVIAPGTPSONTOCQCPPTGESSAS 133  
DB 97 -ASDFVCTCKEQHCTSKDCEACAAQTICPIPGFVGMEMATETDTVCHPCPGVFFSNQS 155  
  
QY 134 SSSEQCPHRRNCTALGLALNVPGSSSHDTLC 164  
DB 156 SLFEKCVPTSCEDKNLEVLQKGTSTQTNVIC 186  
  
RESULT 13  
CD40_BOVIN  
ID CD40_BOVIN STANDARD; PRT; 269 AA.  
AC Q28203;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).  
GN TNFRSF5 OR CD40.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97281252; PubMed=9135560;  
RA Hirano A.; Brown W.C.; Estes D.M.;  
RT "Cloning, expression and biological function of the bovine CD40  
homologue: role in B-lymphocyte growth and differentiation in  
cattle."  
RL Immunology 90:294-300(1997).
```

CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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 CC -----  
 DR EMBL: U57745; AAC48710.1; -;  
 DR HSSP: P25942; 1CDF.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 4.  
 DR ProDom: PD000771; TNFR\_c6; 1.  
 DR SMART: SM00208; TNFR; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE: PS00050; TNFR\_NGFR\_2; 1.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 >269 CD40L RECEPTOR.  
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 194 215 POTENTIAL.  
 FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 187 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 103 TNFR-CYS 2.  
 FT REPEAT 104 144 TNFR-CYS 3.  
 FT REPEAT 145 187 TNFR-CYS 4.  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 269 269  
 SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;  
 Query Match 13.5%; Score 202; DB 1; Length 269;  
 Best Local Similarity 28.5%; Pred. No. 2.6e-09;  
 Matches 67; Conservative 20; Mismatches 122; Indels 26; Gaps 7;  
 QY 18 LVCAQCPGPGTFVQPCRRDSPPTTCGPPRHYTFQFN---YLCRCYCNVLCGEREEA- 73  
 Db 36 LCDLCPGPGKLVNDCTEVSKCQSGKGEFLSTWNREKYCHEHRYCNPNLGLRIQSEG 95  
 QY 74 -----RACHATHNRACRCRTGFFAHAGFCLEHASCPCPGAGVIAPGTPSQTQCPQPGT 128  
 Db 96 TLNTDTICVCEGOHCTSHT-----CESCTPHSLCLPGFGVKQIATGLLDTVCEPCLGF 150  
 QY 129 FSASSSSQCPQRNCTALGLALNVPGSSSHDTLCTSCGFPPLSTRVPGAECERAVID 188  
 Db 151 FSNVSAFAKCHRWTSCKRGLVEQHVGNKTDVVC---GFQSRNRTLVIPIVTMGVLF 206  
 QY 189 VFVAFQDISIKRLQRLQALPAPEGWGPPTPRAGAAQLKLRRL---TELLGAQD 240  
 Db 207 AVLLVSACIRNITKKQ-LRPCTLW-----LGRIPWRRLIRRFPPAPTRLUGARD 256  
 RESULT 14  
 OX40\_MOUSE  
 ID OX40\_MOUSE STANDARD; PRT; 272 AA.  
 AC P47741;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).  
 GN TNFRSF4 OR TXGP1 OR OX40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C;  
 RX MEDLINE=94044750; PubMed=8228223;  
 RA Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,  
 RA Claassen E., Noelle R.J., Fell H.;  
 RT "Cloning of mouse OX40: a T cell activation marker that may mediate  
 RT T-B cell interactions.";  
 RL J. Immunol. 151:5261-5271(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95255413; PubMed=7737295;  
 RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
 RA Barclay A.N.;  
 RT "Gene structure and chromosomal localization of the mouse homologue  
 RT of rat OX40 protein.";  
 RL Eur. J. Immunol. 25:926-930(1995).  
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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 CC -----  
 DR EMBL: Z11674; CAA79772.1; -;  
 DR EMBL: X85214; CAA59476.1; -;  
 DR HSSP: P25942; 1CDF.  
 DR MGD: MGI:104512; Tnfrsf4.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 3.  
 DR ProDom: PD000771; TNFR\_c6; 1.  
 DR SMART: SM00208; TNFR; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS00050; TNFR\_NGFR\_2; 2.  
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
 KW Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 272 OX40L RECEPTOR.  
 FT DOMAIN 20 211 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 212 236 POTENTIAL.  
 FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 26 165 4 X TNFR-CYS.  
 FT REPEAT 26 61 TNFR-CYS 1.  
 FT REPEAT 62 103 TNFR-CYS 2.  
 FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).  
 FT REPEAT 125 165 TNFR-CYS 4.  
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 15 15 A -> G (IN REF. 2).  
 SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;  
 Query Match 13.0%; Score 194.5; DB 1; Length 272;  
 Best Local Similarity 30.4%; Pred. No. 1e-08;  
 Matches 51; Conservative 16; Mismatches 58; Indels 43; Gaps 8;  
 QY 6 TYPWRDAETGERLVCAQCPGPGTFVQPCRRDSPPTTCGPPRHYTFQFN---LERCRYCN 63  
 Db 31 TYP-----SGHK-CCRECQPGHGMVSRCDTRDTLCHPCTGYNEAVNDTKQCTQCN 84  
 QY 64 VLCGEREEARACHATHNRACRTGFFAHAGFCLEHASCPCPGAGVIAPGT-PSQNT--- 119  
 Db 85 HRSG--SELKQNCPTQDTCRCR-----PQTQPRQDSGYK 118  
 QY 120 ---QCPCPPGTFSSSSSESCQCPHRNCTALGLALNVPGSSSHDTLC 164  
 Db 119 LGVDCVPCPPGPHF--SPGNNAQKPKWTNCTLSGKQTRHRPASDILDVAVC 164  
 RESULT 15  
 41BB\_MOUSE

```

SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;

Query Match 12.4%; Score 185; DB 1; Length 256;
Best Local Similarity 28.3%; Pred. No. 5.4e-08;
Matches 65; Conservative 24; Mismatches 85; Indels 56; Gaps

Qy 20 CAQCPCGTFVORPCRRDSPTCGCPPRHYTQFWNYLERCRCYCNVLCGEREEARACHAT 79
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 28 CDNCQPGTF---CRKYNP-VCKSCPSTPSSIGGO-PNCNICRV-CAGYFRFKFCSSST 80
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 80 HNRACRCTGFFAHAGFCLC-HASCPCGAGVIAGTPSQNTQCPCPPGTFSSASSSSEQ 138
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 81 HNAECIEGPHCLGPOCTCEKDCRPGQELTKOG-----CKTCSLGFNF-DQNGTGV 132
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 139 CQPHRNCATGLALNVNPGSSSHDTLCTSCGFPLSTRVPGAECERAVIDFAVQDISIK 198
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 133 CRPWTNCSLDGRSVLKGTTEKDVCV---GPP-----VVVSFSPSTTISV- 173
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 199 RLQRLQALPAEGWGPTPRAGRAALQKLKRLRLTELLGQAQDGAALLRLL 248
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 174 -----TPEG-GP---GGHSLQV-----LTFL-ALTSALLALI 202
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Search completed: May 10, 2002, 10:59:24
Job time: 333 sec

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Search completed: May 10, 2002, 10:59:24  
Job time: 333 sec

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GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: May 10, 2002, 10:54:20 ; Search time 24.1 Seconds  
(without alignments)  
856.569 Million cell updates/sec

Title: US-09-280-567-6  
Perfect score: 1491  
Sequence: 1 VAETTYPRDAETGRLVC.....RVAMPGLSVRRFLPVH 271

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.68.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	340.5	22.8	461	1	A35356 tumor necrosis fac
2	333.5	22.4	459	2	I48854 gene murine tumour
3	332.5	22.3	474	2	B38634 tumor necrosis fac
4	299.5	20.1	435	2	I54182 tumor necrosis fac
5	260	17.4	348	2	T28623 hypothetical prote
6	260	17.4	349	2	D72175 G2R protein - vari
7	260	17.4	349	2	D36858 gene G4R protein -
8	234.5	15.7	325	2	B43692 T2 protein - rabbi
9	215.5	14.5	277	2	I37552 OX40 homolog - hum
10	211.5	14.2	271	2	S12783 OX40 antigen precu
11	211	14.2	277	2	A60771 B-cell activation
12	210.5	14.1	326	1	QOVZML T2 protein - myxom
13	203	13.6	305	2	A46476 B cell-associated
14	194.5	13.0	272	2	I48700 gene ox40 protein
15	185	12.4	256	2	B32393 T-cell antigen 4-1
16	182	12.2	595	2	A42086 CD30 antigen precu
17	174	11.7	255	2	I38426 lymphocyte activat
18	171.5	11.5	416	1	JN0006 nerve growth facto
19	168	11.3	425	1	A26431 nerve growth facto
20	158	10.6	427	1	GQHUN nerve growth facto
21	155.5	10.4	327	2	A46484 apoptosis-mediati
22	148.5	10.0	1574	2	T13954 MEGF6 protein - ra
23	148	9.9	250	1	A49053 CD27 antigen precu
24	147.5	9.9	5376	1	T42215 zonadhesin - mouse
25	146.5	9.8	260	1	A46517 CD27 antigen precu
26	145	9.7	335	2	A40036 apoptosis-mediati
27	143	9.6	1620	2	T27283 hypothetical prote
28	140	9.4	314	2	I37383 Fas soluble protei
29	137.5	9.2	324	2	JC2395 Fas antigen precu

30 135.5 9.1 1299 2 T43251 furin (EC 3.4.21.7  
31 135 9.1 2321 2 S78549 notch3 protein - h  
32 130.5 8.8 454 1 GQMST1 tumor necrosis fac  
33 128.5 8.6 3635 2 T10053 laminin alpha 5 ch  
34 127 8.5 1192 2 S69000 laminin gamma 2 ch  
35 125.5 8.4 1548 2 S34583 serine proteinase  
36 124.5 8.4 1713 2 A55347 adhesive ligand ep  
37 123.5 8.3 455 1 GQHUT1 tumor necrosis fac  
38 123.5 8.3 493 2 JC5486 membrane glycoprot  
39 122.5 8.2 2824 2 T22759 hypothetical prote  
40 121 8.1 3106 1 S53868 laminin alpha-2 ch  
41 120 8.0 1609 1 MMHUR2 laminin gamma-1 ch  
42 119.5 8.0 3084 1 MMMSA laminin alpha-1 ch  
43 118.5 7.9 461 1 GQRTT1 laminin alpha-1 ch  
44 118.5 7.9 1680 2 A43434 tumor necrosis fac  
45 118 7.9 899 2 G02428 furin (EC 3.4.21.7  
subtilisin-like pr

## ALIGNMENTS

## RESULT 1

A35356  
tumor necrosis factor receptor 2 precursor [validated] - human  
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000  
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990  
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular a  
A:Reference number: A35356; MUID:90260639  
A:Accession: A35356  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <SM>  
A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186  
R:Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc  
A:Reference number: A36475; MUID:91045991  
A:Accession: A36475  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195; 'R', 197-461 <KOH>  
A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758  
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990  
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular  
A:Reference number: A48416; MUID:91370690  
A:Accession: A48416  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 23-461 <DEM>  
A:Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649  
A:Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIF:63371)  
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons  
A:Reference number: A36007; MUID:90349572  
A:Accession: A36007  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 116-140; 'p', 142-195; 'R', 197-362; 'T', 364-461 <HEL>  
A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752  
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990  
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor  
A:Reference number: A23666; MUID:91056048  
A:Accession: A23666  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>

R;Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
A;Reference number: A35010; MUID:90110215  
A;Accession: B35010  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 27-31 <ENG>  
R;Kuhnert, P.; Kemper, O.; Wallach, D.  
Gene 150, 381-386, 1994  
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of  
A;Reference number: I38094; MUID:95121934  
A;Accession: I38094  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-37 <RES>  
A;Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701  
C;Genetics:  
A;Gene: GDB:TNFR2  
A;Cross-references: GDB:l125914; OMIM:191191  
A;Map position: lp36.2-lp36.2  
A;Introns: 26/3  
A;Note: the list of introns is incomplete  
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>  
F;40-76/Domain: NGF receptor repeat homology <NG1>  
F;78-119/Domain: NGF receptor repeat homology <NG2>  
F;120-162/Domain: NGF receptor repeat homology <NG3>  
F;164-201/Domain: NGF receptor repeat homology <NG4>  
F;262-279/Domain: transmembrane #status predicted <TMN>  
F;280-461/Domain: intracellular #status predicted <INT>  
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.8%; Score 340.5; DB 1; Length 461;  
Best Local Similarity 29.7%; Pred. No. 1.3e-18;  
Matches 89; Conservative 43; Mismatches 115; Indels 53; Gaps 11;

Qy 1 VAETPTYPWRDAETGE-----RLVCAQCPGTFVQRPCRDSPPTCGPCPRH 48  
Db 27 VAFTYAP-----EPGSCRLREYDQTAQCCSKCSGQHAKEVCTKTSVTCDSCEDET 82  
Qy 49 YTFWNLYRCRYCNVLGEBREEPARACHATHNRACRRTGFFAHAG-----FCLHAS 102  
Db 83 YTQLNNVWPECLSCGSCSSDQVETOACTREQNRICTRCPGWCALSKQECRCAPLRK 142  
Qy 103 CPPGAGVIAGTPSONTCQPCPGTFSASSSEQCPHNRCTALGLALNVPSSSHDT 162  
Db 143 CRPGFGVAREGTETSDVYCKPCAPGTFSNTSTSDICRPHQICNVVA-----IPGNASMDA 198  
Qy 163 LCSTCGFLPSTRVPAGEECERAVDFVAFQDISIKRLQLQALEAPE-----GWGPTP 217  
Db 199 VCRSTS--PFRMAPGAVHLPQV-----STRSQHTQTPPESTAPSTFLLPMGSP 249  
Qy 218 RA-----GRAALQLKRLRLTELLGAODGALLVRLQLAL---RVARMP-GLERSVRERFLP 269  
Db 250 PAEGSTGDFALPVGLIVGVTA-----GLLIIGVNCVINTQVKKKFLCLQREAKVPHLP 304

RESULT 2  
I48854  
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999  
C;Accession: I48854  
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.  
Mamm. Genome 5, 726-727, 1994  
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
A;Reference number: I48854; MUID:95178848  
A;Accession: I48854  
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA  
A;Residues: 1-459 <RES>  
A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831  
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
F;151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 22.4%; Score 333.5; DB 2; Length 459;  
Best Local Similarity 29.7%; Pred. No. 4.5e-18;  
Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps 9;

Qy 17 RLVCAQCPGTFVQRPCRDSPPTCGPCPRHYTFQWNYLRCRYCNVLGEREEARAC 76  
Db 37 QMCAKCPGQGVYKHFCKNTSDTVCADEASMYTQVWQNFRTCLSCSSCSCTDQVETRAC 96  
Qy 77 HATHNRACRCTGTF-----AHAGF---CLEHASCPGPGAGVIAGTPSONTCQPCPGT 129  
Db 97 TKQNRVCAACBAGRYCALKTHSGSCRCQCMRLSKGPGFVASSRAPNGNVLCACAPTF 156  
Qy 130 SASSSSSEQCPHNRCTALGLALNVPSSSHDTLCT-----SCTGFPLSTRVPAGEECERA 185  
Db 157 SDTTSSTDVCRPHRCSILA----IPGNASTDAVCAPESPTLSAIPRFLYVSQEPETRSQ 212  
Qy 186 VIDFVAFQDISIKRLQLQALEAPEGWGPTP-----RAGRAALQLKRLRLTELLGAOD 240  
Db 213 PLD-----QEPGSPQTPSILTSL-----GSTPIIEQSTKGGISLPIGLIVGVTSL----- 257  
Qy 241 GALLVRLQLAL---RVARMPGLERSVRERFLP 269  
Db 258 GLLMLGLVNCFILVORKKPKSCLQORDAKRVHPV 290

RESULT 3  
B38634  
tumor necrosis factor receptor type 2 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
C;Accession: B38634; A40254; S54816  
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,  
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto  
A;Reference number: A38634; MUID:91187885  
A;Accession: B38634  
A;Molecule type: mRNA  
A;Residues: 1-474 <LEW>  
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J  
Mol. Cell. Biol. 11, 3020-3026, 1991  
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f  
A;Reference number: A40254; MUID:91246168  
A;Accession: A40254  
A;Molecule type: mRNA  
A;Residues: 1-474 <GOO>  
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
R;Kisssonergis, M.; Fallowes, R.; Feidmann, M.; Chernajovsky, Y.  
submitted to the EMBL Data Library, May 1995  
A;Description: Characterization of the promoter region of the murine p75-TNF receptor  
A;Reference number: S54816  
A;Accession: S54816  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-22 <KIS>  
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044  
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C;Keywords: cytokine receptor; transmembrane protein  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
F;40-77/Domain: NGF receptor repeat homology <NG1>  
F;79-120/Domain: NGF receptor repeat homology <NG2>  
F;166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 22.3%; Score 332.5; DB 2; Length 474;

R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; A Nature 366, 748-751, 1993

A;Title: Potential virulence determinants in terminal regions of variola smallpox virus  
A;Reference number: Z20488; MUID:94088747  
A;Accession: T28623  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-348 <NMA>  
A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102  
A;Experimental source: strain Bangladesh 1975  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 260; DB 2; Length 348;  
Best Local Similarity 32.2%; Pred. No. 1.3e-12;  
Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

Qy 5 PTYWRDAE-TGERLVCAQCPPGTFVORPCRRDSPITTCGPCPRPHYTOFWNYLERCRYCN 63  
Db 27 PNGKCKDETKYKRHNLCCLSCPPGYASRLCDSKTNTQCTPCGGSGTFTSRNNHLPACLSCN 86  
Qy 64 VLGGEREEARACHATHNRACRCRTGF-----AHAGFCLEHASCPPGAGVIAPGTPSQ 117  
Db 87 GRCSNQVEFRSCNTNHRIECSPGYCYLLKGSSGCKACVSQTCKGIGYGV-SGHTSVG 145  
Qy 118 NTQCQPCCPPTFSASSSSSQOCPHRNCTALGLNALNVGPSSTDTLTCTCGTPLSTRVP 177  
Db 146 DVICSPCGFGTYSHTVSSADKCEPVNPNTENYIDVEITLYPVNDTSCTRTTTGLSESIL 205  
Qy 178 GAE 180  
Db 206 TSE 208

RESULT 6  
D72175  
G2R protein - variola minor virus (strain Garcia-1966)  
C:Species: variola minor virus  
C>Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 20-Jun-2000  
C:Accession: D72175  
R:Scheikunov, S.N.; Totmenin, A.V.; Guttorov, V.V.; Safronov, P.F.; Massung, R.F.; Lo submitted to Genbank, March 1998  
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola m  
A:Reference number: A72150  
A:Accession: D72175  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-349 <SHC>  
A;Cross-references: GB:X16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759  
A;Experimental source: strain Garcia-1966  
C:Genetics:  
A:Gene: G2R  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 260; DB 2; Length 349;  
Best Local Similarity 32.2%; Pred. No. 1.3e-12;  
Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

Qy 5 PTYWRDAE-TGERLVCAQCPPGTFVORPCRRDSPITTCGPCPRPHYTOFWNYLERCRYCN 63  
Db 28 PNGKCKDETKYKRHNLCCLSCPPGYASRLCDSKTNTQCTPCGGSGTFTSRNNHLPACLSCN 87  
Qy 64 VLGGEREEARACHATHNRACRCRTGF-----AHAGFCLEHASCPPGAGVIAPGTPSQ 117  
Db 88 GRCSNQVEFRSCNTNHRIECSPGYCYLLKGSSGCKACVSQTCKGIGYGV-SGHTSVG 146  
Qy 118 NTQCQPCCPPTFSASSSSSQOCPHRNCTALGLNALNVGPSSTDTLTCTCGTPLSTRVP 177  
Db 147 DVICSPCGFGTYSHTVSSADKCEPVNPNTENYIDVEITLYPVNDTSCTRTTTGLSESIL 206  
Qy 178 GAE 180  
Db 206 TSE 208

Db 207 TSE 209

## RESULT 7

D36858 gene G4R protein - variola virus

N;Alternate names: B28R protein (COP)

C;Species: variola virus

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 23-Mar-2001

A;Accession: D36858; S46858; S32385; S35987

R;Blinov, V.M.

submitted to GenBank, November 1992

A;Reference number: A36859

A;Accession: D36858

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-349 &lt;BLI&gt;

A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087

A;Experimental source: strain India-1967, ssp. major, isolate ind3

R;Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, V.V.

submitted to the EMBL Data Library, April 1992

A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P

A;Reference number: S46868

A;Accession: S46888

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-349 &lt;ROL&gt;

A;Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449

A;Experimental source: strain India-1967, isolate ind3

R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.

FEBS Lett. 319, 80-83, 1993

A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective

A;Reference number: S32385; MUID:93202281

A;Accession: S32385

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-168 &lt;SHC&gt;

A;Cross-references: EMBL:X69198

A;Experimental source: strain India-1967, ssp. major

C;Genetics:

A;Gene: G4R

C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

F;32-66/Domain: NGF receptor repeat homology &lt;NGF&gt;

F;68-109/Domain: NGF receptor repeat homology &lt;NG3&gt;

F;110-151/Domain: NGF receptor repeat homology &lt;NG3&gt;

Query Match 17.4%; Score 260; DB 2; Length 349;

Best Local Similarity 32.2%; Pred. No. 1.3e-12;

Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

QY 5 PTYPWRDAE-TGERLVCAQCPPGTFVQRPCCRDSPTTCGPPRRHYTFQWNYLERCRYCN 63

Db 28 PNGKCKDTEYKRNLCLSCPPGYASRLCDSKTNTQCTPGSGSTFTSRNHLPACLSCN 87

QY 64 VLGGEREEARACHATHNRACRGTGFF-----AAGFCLEHASCPPGAGVIAPGTPSQ 117

Db 88 GRNSNQVETRSCNTTHNRICEGSPGYICLLKSGSSGKACVSKTCGIGYGV-SGHTSVG 146

QY 118 NTCQCPGCTTFSSASSSSEOCQPHRNCNTALGLALNVPGSSSHDTLTCTGCTGFPPLSTRVP 177

Db 147 DVTCSPGCGFTYSHTVSSADKCEPVNPNFNYIDVEITLYPVNDTCTRTTTTGLSESIL 206

QY 178 GAE 180

Db 207 TSE 209

## RESULT 8

B43692

T2 protein - rabbit fibroma virus

C;Species: rabbit fibroma virus, Shope fibroma virus

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: B43692

R;Upton, C.; DeLange, A.M.; McFadden, G.

Virology 160, 20-30, 1987

A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomer

A;Reference number: A43692; MUID:87321103

A;Accession: B43692

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-325 &lt;UPT&gt;

A;Cross-references: GB:M17433

C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

F;64-105/Domain: NGF receptor repeat homology &lt;NG2&gt;

F;106-147/Domain: NGF receptor repeat homology &lt;NG3&gt;

Query Match 15.7%; Score 234.5; DB 2; Length 325;

Best Local Similarity 32.9%; Pred. No. 1e-10;

Matches 52; Conservative 19; Mismatches 76; Indels 11; Gaps 3;

QY 18 LVCAQCPPGTFVQRPCCRDSPTTCGPPRRHYTFQWNYLERCRYCNVLCGEREEARACH 77

Db 38 LCCASCHPGFYASRLCGPSTVCSPCEDGTFTASTNHAPACVSCRGPGCTGHLSESQPCD 97

QY 78 ATHNRACRGTGFFA-----HAGFCLEHASCPPGAGVIAPGTPSQNTQCPGPTFSA 131

Db 98 RTHDRVNCSTGNYCLLKGGNGCRICAPQTKCPAGYGV-SGHTRAGDTLCKECPHTYSD 156

QY 132 SSSSEOCQPHRNCNTALGLALNVPGSSSHDTLTCTCTG 169

Db 157 SLSPTERCGTFNYSVIGFNL----YVPNETSCITTAG 190

## RESULT 9

I37552

OX40 homolog - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000

C;Accession: I37552

R;Latza, U.; Durrkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo

Eur. J. Immunol. 24, 677-683, 1994

A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment

A;Reference number: I37552; MUID:94170844

A;Accession: I37552

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-277 &lt;RES&gt;

A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958

C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 14.5%; Score 215.5; DB 2; Length 277;

Best Local Similarity 27.0%; Pred. No. 2.4e-09;

Matches 72; Conservative 22; Mismatches 104; Indels 69; Gaps 11;

QY 6 TYPRWDAETGERLVCAQCPPGTFVQRPCCRDSPTTCGPPRRHYTFQWNY--LERCRYCN 63

Db 35 TYPNSDR-----CCHCEPFGNGMVSRCSQNTQVCPGPGFYNDVYVSKPKCKPCTWCN 88

QY 64 VLGGEREEARACHATHNRACRGTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCP 123

Db 89 LRSG--SERKQLCTATQDTCRCRAG-----TOPLDSYKPG-----VDCAP 127

QY 124 CPGTFSASSSSSEOCQPHRNCNTALGLALNVPGSSSHDTLTCTGCTGFPPLSTRVPGA 180

Db 128 CPPGHF--SPGDNOACKPWTNCTLAGKHTLQPASNSSDAICEDRDPATQPTQGGPAR 185

QY 181 ECERAVIDFVAFQDISIKRLQRLQLEAPEGW-----GTPPR-----AGRAALQLKLR 230

Db 186 PI-----TVQPTAMPRTSQSPSTRPVEVPGGRAVAAILGLG 222

QY 231 RLTELLGAQDGALLVRLQLQALRVAMP 257

Db 223 LVLLGLGLPL--AILLALLYLLRRQRLP 247



F:216-277/Domain: intracellular #status predicted <C>  
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match          14.2%; Score 211; DB 2; Length 277;
Best Local Similarity 30.5%; Pred. No. 5.3e-09;
Matches              46; Conservative 21; Mismatches 76; Indels 8; Gaps 3;
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QY 20 CAQCPCGTFVORPCRDRSPITCGCPPRHHYTQFNWYLERC---RYCNVLGEREEERARAC 76  
| : | | | : | : | | : | : | : | : | : | : | : | : |  
Db 38 CSLCQPQCKLVSDCTETETECPLCGSEFLDTWNRETHCHQHKKYCDPNLGLRVQQKGT 97  
| : | : | : | : | : | : | : | : | : | : | : | : | : |  
QY 77 HATHNRACRRTGFFAHA---GFCLEHASPGGAGVIAPGTPSONTOQCPCPPGTFSSASS 133  
| : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 98 ET--DTICTCEGHWCSTSEACESCVLRHSRSGFGVKQIATGVSDTICEPCPGVFSSNVS 155  
| : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 134 SSSDQCOPHRNCTALGLALNPVGSSSHDTLC 164  
| : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 156 SAFEKCHKPWTSCETKDLVVQAAGTKNDVVC 186  
| : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 12  
GVQZML  
T2 protein - myxoma virus (strain Lausanne)  
C:Species: myxoma virus  
C:Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 18-Jun-1999  
C:Accession: A40566  
R;Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.  
Virolgy 184, 370-382, 1991  
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor receptor  
A:Reference number: A40566; MUID:91335768  
A:Accession: A40566  
A:Molecule type: DNA  
A:Residues: 1-326 <UPT>  
A:CROSS-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
C:Keywords: glycoprotein  
F:64-105/Domain: NGF receptor repeat homology <NG2>  
F:106-147/Domain: NGF receptor repeat homology <NG3>  
F:66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.1%; Score 210.5; DB 1; Length 326;  
Best Local Similarity 30.4%; Pred. No. 6.7e-09;  
Matches 48; Conservative 19; Mismatches 80; Indels 11; Gaps 3;

QY 18 LVCAQCPCGTFVQRCRRDSPITTCGCPPRHYTQFNWYLERCRCYNVLCGEREEERACH 77  
| : | | | | : | : | : | : | : | : | : | : | : | : |  
Db 38 LCCTSPPGYASRLCGPGSDTVCSCKNETFTASTNHAPACVSCRGCTCHLSESQSCD 97  
| : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 78 ATHNRACRRTGFPA-----HAGFCLHEASCPGAGVIAPGTPSONTOQCPCPPGTFSA 131  
| : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 98 KTRDRVDCSAGNYCLLKGBGCRICAPKPKPAGYGV-SGHTRTGDVLTKCPRYTVD 156  
| : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 132 SSSSEOCQPHRNCTALGLANVPVGSSSHDFLTCTSC TG 169  
| : | | | | : | : | : | : | : | : | : | : | : | : |  
Db 157 AVSSTECTSFNFISVEFNL----YPVNDYFCTTTAG 190  
| : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 13  
A46476  
B call-associated surface molecule CD40, long splice form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
C:Accession: A46476; A46515  
R;Torres, R.M.; Clark, E.A.  
J. Immunol. 148, 620-626, 1992  
A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine B cell-associated surface molecule CD40  
A:Reference number: A46476; MUID:92105763  
A:Accession: A46476  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-305 <TOR>

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Qy 6 TYPRDAETGERLVACQPPGTFVQRCDRSDPTTCGCPPRHYTFQWNY---LERCRCYN 63
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
Db 31 TYP-----SGHK--CCRECPGPGHGMWRCRDHTRDTLCHPCETGTYNEAVNYDTCKQCTQCN 84

Qy 64 VLCGEREEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGT-PSQNT--- 119
   | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 85 HRSG--SELKQNTPTQDTVTCRCR-----PGTQPRODSGYK 118

Qy 120 ---QCQCPGPTGSASSSEOCQPHRNCTALGLALNVPSSSHDTLC 164
   ||||| ||| : : : : ||| : | | | | | | | | | | | | | | | | | | | |
Db 119 LGVDVCPGPGHF--SPGNQACKPWTNCTLSGKQTRHPASDSDAVC 164

RESULT
B32393
C:cell antigen 4-1BB precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C:Accession: B32393; I48879
R:Kwon, B.S.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
A:title: cDNA sequence of two inducible T-cell genes.
A:Reference number: A32393; MUID:89184547
A:Accession: B32393
A:Molecule type: mRNA
A:Residues: 1-256 <KW>
A:Cross-references: GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.
J. Immunol. 152, 2256-2262, 1994
A:title: Genomic Organization and Chromosomal Localization of the T-Cell A4
A:Reference number: I48879; MUID:94179805
A:Accession: I48879
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-256 <RES>
A:Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178
C:Genetics: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-256/Product: 4-1BB protein #status predicted <WAT>

Query Match 12.4%; Score 185; DB 2; Length 256;
Best Local Similarity 28.3%; Pred. No. 4.5e-07;
Matches 65; Conservative 24; Mismatches 85; Indels 56; Gaps

Qy 20 CAQCPGTFVQRCDRSDPTTCGCPPRHYTFQWNYLRCRCVNLGCGEREERACHAT 79
   ||| ||||| |||| : ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 28 CDMCQPGTF---CRKYNP-VCKSCPSTFSIGGQ-PMCNLCRV-CAGYFRFKFCST 80

Qy 80 HNRACRCRTGFFAHAGFCLE-HASCPGAGVIAPTGTPSONTQCQPPGTFSSASSSEQ 138
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 81 HNAECEIEGFHCLGPQCRCCKDCRPGQELTKQG-----CKTCSLGTEN-DQNGTGV 132

Qy 139 CQPHRNCTALGLALNVPSSSHDTLTCTSGTPLSTRVPGAECEBRAVIDFVAFODISIK 198
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 133 CRPWTCNSLDGRSVLTGTGTEKDVVC---GPP-----VVSFSPSTTISV- 173

Qy 199 RLQRLQALAEPEGWGPTPRAGRAALQKLRRRLTELLGAGDQALLVRL 248
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 174 -----TPEG-GP-----GCHSLQV-----LTLFL-ALTSALLLALI 202

Search completed: May 10, 2002, 10:54:21

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Search completed: May 10, 2002, 10:54:21  
Job time: 110 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 10, 2002, 10:53:03 ; Search time 22.98 Seconds  
(without alignments)  
265.378 Million cell updates/sec

Title: US-09-280-567-6  
Perfect score: 1491  
Sequence: 1 VASTPPWRDAETGERLVC.....RVAMPGLERSVREPLVH 271

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A-COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B-COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A-COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B-COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS-COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1491	100.0	300	2	US-08-794-796-2
2	1476.5	99.0	299	4	US-09-286-529-17
3	1034	69.3	211	4	US-09-286-529-20
4	841	56.4	153	4	US-09-286-529-2
5	440.5	29.5	401	3	US-08-974-022-6
6	440.5	29.5	401	4	US-09-042-785A-12
7	440.5	29.5	401	4	US-08-795-445A-6
8	440.5	29.5	401	4	US-08-795-447A-6
9	440.5	29.5	401	4	US-08-974-186-6
10	440.5	29.5	401	4	US-08-795-446B-6
11	440.5	29.5	401	4	US-09-153-927-1
12	425.5	28.5	401	3	US-08-974-022-2
13	425.5	28.5	401	4	US-08-795-445A-2
14	425.5	28.5	401	4	US-08-795-447A-2
15	425.5	28.5	401	4	US-08-974-186-2
16	425.5	28.5	401	4	US-08-795-446B-2
17	424.5	28.5	401	3	US-08-974-022-4
18	424.5	28.5	401	4	US-09-042-785A-13
19	424.5	28.5	401	4	US-08-795-445A-4
20	424.5	28.5	401	4	US-08-795-447A-4
21	424.5	28.5	401	4	US-08-974-186-4
22	424.5	28.5	401	4	US-08-795-446B-4
23	342.5	23.0	461	4	US-09-042-785A-7
24	342.5	23.0	461	4	US-09-006-353A-4
25	340.5	22.8	461	1	US-08-385-229-2
26	340.5	22.8	461	2	US-08-650-000-2
27	340.5	22.8	461	4	US-08-477-347-3

Query Match 100.0% Score 1491; DB 2; Length 300;

28 340.5 22.8 461 4 US-08-476-862-2 Sequence 2, Appli  
29 340.5 22.8 461 6 5395760-2 Patent No. 5395760  
30 335 22.5 227 3 US-08-974-022-48 Sequence 48, Appl  
31 335 22.5 227 4 US-08-795-445A-48 Sequence 48, Appl  
32 335 22.5 227 4 US-08-795-447A-48 Sequence 48, Appl  
33 335 22.5 227 4 US-08-974-186-48 Sequence 48, Appl  
34 335 22.5 227 4 US-08-795-446B-48 Sequence 48, Appl  
35 335 22.5 235 4 US-09-326-394-4 Sequence 4, Appl  
36 333 22.3 486 1 US-08-243-010-1 Sequence 1, Appl  
37 333 22.3 518 1 US-08-385-229-4 Sequence 4, Appl  
38 332.5 22.3 474 2 US-08-650-000-4 Sequence 8, Appl  
39 332.5 22.3 474 4 US-09-042-785A-8 Patent No. 5395760  
40 332.5 22.3 474 6 5395760-4 Sequence 5, Appl  
41 318 21.3 163 2 US-08-219-237B-5 Sequence 13, Appl  
42 318 21.3 163 4 US-08-477-347-13 Sequence 4, Appl  
43 318 21.3 163 4 US-08-476-862-4 Sequence 5, Appl  
44 318 21.3 163 4 US-08-468-560C-5 Sequence 9, Appl  
45 316 21.2 164 2 US-08-232-087A-9

#### ALIGNMENTS

RESULT 1  
US-08-794-796-2  
; Sequence 2, Application US/08794796  
; Patent No. 5885800  
; GENERAL INFORMATION:  
; APPLICANT: Emery, John  
; APPLICANT: Tan, KB  
; APPLICANT: Truneh, Alem  
; APPLICANT: Young, Peter  
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,  
; TITLE OF INVENTION: TR4  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/794,796  
; FILING DATE: 04-FEB-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Han, William T  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: GH50000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-4026  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 300 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-794-796-2

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Best Local Similarity 100.0%; Pred. No. 2.3e-124;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPGTFVORPCRRDSTTCGCPPRHYTQFWNYLERCR 60
DB 30 VAETPTYPWRDAETGERLVCAQCPGTFVORPCRRDSTTCGCPPRHYTQFWNYLERCR 89
QY 61 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTPSQNTQ 120
DB 90 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTPSQNTQ 149
QY 121 CQCPGPGTFSASSSEQCQPHRNCNTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 180
DB 150 CQCPGPGTFSASSSEQCQPHRNCNTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 209
QY 181 ECERAVIDFVAFQDISIKRLQLLALEAPEGWGTPPRAGRAALQKLRRRLTELLGAQD 240
DB 210 ECERAVIDFVAFQDISIKRLQLLALEAPEGWGTPPRAGRAALQKLRRRLTELLGAQD 269
QY 241 GALLVRLQLALRVARMPGLERSVREERFLPVH 271
DB 270 GALLVRLQLALRVARMPGLERSVREERFLPVH 300

RESULT 2
US-09-286-529-17
; Sequence 17, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286.529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-17

Query Match 99.0%; Score 1476.5; DB 4; Length 299;
Best Local Similarity 99.6%; Pred. No. 4.4e-123;
Matches 270; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VAETPTYPWRDAETGERLVCAQCPGTFVORPCRRDSTTCGCPPRHYTQFWNYLERCR 60
DB 30 VAETPTYPWRDAETGERLVCAQCPGTFVORPCRRDSTTCGCPPRHYTQFWNYLERCR 89
QY 61 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTPSQNTQ 120
DB 90 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTPSQNTQ 149
QY 121 CQCPGPGTFSASSSEQCQPHRNCNTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 180
DB 150 CQCPGPGTFSASSSEQCQPHRNCNTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 208
QY 181 ECERAVIDFVAFQDISIKRLQLLALEAPEGWGTPPRAGRAALQKLRRRLTELLGAQD 240
DB 209 ECERAVIDFVAFQDISIKRLQLLALEAPEGWGTPPRAGRAALQKLRRRLTELLGAQD 268
QY 241 GALLVRLQLALRVARMPGLERSVREERFLPVH 271
DB 269 GALLVRLQLALRVARMPGLERSVREERFLPVH 299

RESULT 3
US-09-286-529-20
; Sequence 20, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
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; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286.529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-20

Query Match 69.3%; Score 1034; DB 4; Length 211;
Best Local Similarity 98.9%; Pred. No. 3.7e-84;
Matches 179; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPGTFVORPCRRDSTTCGCPPRHYTQFWNYLERCR 60
DB 30 VAETPTYPWRDAETGERLVCAQCPGTFVORPCRRDSTTCGCPPRHYTQFWNYLERCR 89
QY 61 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTPSQNTQ 120
DB 90 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTPSQNTQ 149
QY 121 CQCPGPGTFSASSSEQCQPHRNCNTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 180
DB 150 CQCPGPGTFSASSSEQCQPHRNCNTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 209
QY 181 E 181
DB 210 E 210

RESULT 4
US-09-286-529-2
; Sequence 2, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286.529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 153
; TYPE: PRT
; ORGANISM: human
US-09-286-529-2

Query Match 56.4%; Score 841; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.9e-67;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 LERCYCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTP 115
DB 1 LERCYCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPCGAGVIAPGTP 60
QY 116 SONTQCQCPGPGTFSASSSEQCQPHRNCNTALGLALNVPGSSSHDTLCTSGTGFPLSTR 175
DB 61 SONTQCQCPGPGTFSASSSEQCQPHRNCNTALGLALNVPGSSSHDTLCTSGTGFPLSTR 120
QY 176 VPGAEECERAVIDFVAFQDISIKRLQLLALE 208
DB 121 VPGAEECERAVIDFVAFQDISIKRLQLLALE 153

RESULT 5
US-08-974-022-6
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: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109
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: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/042,785A
: FILING DATE: 17-MAR-1998
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/938,896
: FILING DATE: 26-SEP-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Mandragoras, Amy E
: REGISTRATION NUMBER: 36,207
: REFERENCE/DOCKET NUMBER: MEI-001CP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)742-4214
:
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 401 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
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: US-09-042-785A-12
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: Best Local Similarity 41.2%; Pred. No. 2.3e-31;
: Matches 77; Conservative 31; Mismatches 74;
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: Db 26 PKYLHYDEETSHOLLKDCKCPGPTYLKQHCTAKWKTVCAPCDPDYH
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: QY 65 LCGEREERARACHATHNRACRGTGFGFAHAGCLERHASCPGPGAG
: Db 86 VKLEQYVQECNRTHNRVCECKEGRYLEIFCLKHRSCPPGPGF
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: QY 125 PPGTFSASSSSBQCOPHRNCKTALGLALNVPGSSSHDTLCTCTCT
: Db 146 PDGFFSNFTSSKAPCRKHNTCSVFGLLLTQGNATHDNI--CS
:
: QY 183 ERAVIDF 189
: Db 203 EEAFFR 209
:
: RESULT 7
: US-08-795-445A-6
: Sequence 6, Application US/08795445A
: Patent No. 6284485
: GENERAL INFORMATION:
: APPLICANT: Boyle, William J.
: APPLICANT: Lacey, David L.
: APPLICANT: Calzone, Frank J.
: APPLICANT: Chang, Ming-Shi
: TITLE OF INVENTION: OSTEOPROTEGERIN
: NUMBER OF SEQUENCES: 53
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Amgen Inc.
: STREET: 1840 Behavliand Drive
: CITY: Thousand Oaks
: STATE: California
: COUNTRY: USA
: ZIP: 91320-1789
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

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REFERENCE/DOCKET NUMBER: A-378D

Query Match

29.5%; Score 440.5; DB 4; Length 401;



ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-022-2

Query Match 28.5%; Score 425.5; DB 3; Length 401;  
Best Local Similarity 39.5%; Pred. No. 4.9e-30;  
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;  
QY 5 PTPWRDAETGERLVCACQCPPTGTFVORPCRRDSTTCGCPPRHYTOFWNLYLRCRYCNV 64  
DB 26 PKYLHYDPTETGROLCDKCAPGYLKHQCTVRRKTLCLVPCPDYSYDTSWHTSDECVYCS 85  
QY 65 LCGEREEERACHATHNRACRGTGFFAHAGFCLEHASCPPGAGVIAPCTPSQNTQCPC 124  
DB 86 VKLELQTVKQECNRKTHNRVCECEEGRYLEFCLKHRSCTPPGLGLVQAGTPERTVCKRC 145  
QY 125 PPGTFFSASSSSQCPHRCNTALGLALNVPSSSHDTLCTCTGFPPLSTRVPGAEE--C 182  
DB 146 PDGFFSGETSSKAPCRKHTNCSSLLGLLLIQKGNATHDNV---CSGNREATQNGCIDVTLC 202  
QY 183 ERAVIDFAVFQDISIKRLQLQAL 207  
DB 203 EEAFFRFAVPTKIIPNWLVSLL 227

RESULT 13  
US-08-795-445A-2  
Sequence 2, Application US/08795445A  
Patent No. 6284485  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Behavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,445A  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-445A-2  
Query Match 28.5%; Score 425.5; DB 4; Length 401;  
Best Local Similarity 39.5%; Pred. No. 4.9e-30;  
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;  
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DB 26 PKYLHYDPTETGROLCDKCAPGYLKHQCTVRRKTLCLVPCPDYSYDTSWHTSDECVYCS 85  
QY 65 LCGEREEERACHATHNRACRGTGFFAHAGFCLEHASCPPGAGVIAPCTPSQNTQCPC 124  
DB 86 VKLELQTVKQECNRKTHNRVCECEEGRYLEFCLKHRSCTPPGLGLVQAGTPERTVCKRC 145  
QY 125 PPGTFFSASSSSQCPHRCNTALGLALNVPSSSHDTLCTCTGFPPLSTRVPGAEE--C 182  
DB 146 PDGFFSGETSSKAPCRKHTNCSSLLGLLLIQKGNATHDNV---CSGNREATQNGCIDVTLC 202  
QY 183 ERAVIDFAVFQDISIKRLQLQAL 207  
DB 203 EEAFFRFAVPTKIIPNWLVSLL 227

RESULT 14  
US-08-795-447A-2  
Sequence 2, Application US/08795447A  
Patent No. 6284728  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: Osteoprotegerin  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: One Amgen Center Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91362-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,447A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378D2  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-447A-2



Query Match 28.5%; Score 425.5; DB 4; Length 401;  
Best Local Similarity 39.5%; Pred. No. 4.9e-30;  
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DB 203 EEAFFRFAVPTKIIPNWLVLVDLSL 227

RESULT 15  
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; Sequence 2, Application US/08974186  
; Patent No. 6284740  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Behavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,186  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 401 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-974-186-2

Query Match 28.5%; Score 425.5; DB 4; Length 401;  
Best Local Similarity 39.5%; Pred. No. 4.9e-30;  
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;  
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QY 65 LCGEREEARACHATHNRACRRTGFFAHAGFCLEHASCPGAGVIAPGTPSONTQOCP 124  
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QY 125 PPGTFSASSSSQCOQPHRNCRTALGLALNVPSSSHDTLTCTSGTGPLSTRVPGAEE--C 182  
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DB 203 EEAFFRFAVPTKIIPNWLVLVDLSL 227

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Copyright (c) 1993 - 2000 CompuGen Ltd.  
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(without alignments)  
499.847 Million cell updates/sec

Title: US-09-280-567-6  
Perfect score: 1491  
Sequence: 1 VAETPTVWRDAETGERLVC.....RVAMPGLERSVRERFLPVH 271

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Gapop 10.0 , Gapext 0.5  
Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length DB	ID	Description
1	1491	100.0	271	20	AA42184 Human mFLINT #1 pr
2	1491	100.0	271	21	AA19334 A mature human FAS
3	1491	100.0	271	21	AA19705 Human FAS ligand i
4	1491	100.0	271	21	AA97247 M68 TNF receptor r
5	1491	100.0	271	21	AA96598 Human mature FLINT
6	1491	100.0	271	22	AAE03567 Human mature fas l
7	1491	100.0	271	22	AA68044 Amino acid sequenc
8	1491	100.0	271	22	AA68047 Human FLINT mature
9	1491	100.0	271	22	AA68045 Amino acid sequenc
10	1491	100.0	300	19	AAW66102 Human tumour necro
11	1491	100.0	300	19	AAW63622

12	1491	100.0	300	20	AA903099 Human lung TNF-rec
13	1491	100.0	300	20	AA42182 Human FLINT #1 pro
14	1491	100.0	300	20	AA17479 Mammalian tumour n
15	1491	100.0	300	20	AA96817 Human Dcr3 polypep
16	1491	100.0	300	20	AA97749 Human tumour necro
17	1491	100.0	300	20	AAW95082 Orphan receptor (H
18	1491	100.0	300	21	AA19335 A full length huma
19	1491	100.0	300	21	AA28559 Human soluble TNF
20	1491	100.0	300	21	AA24057 Human PRO212 prote
21	1491	100.0	300	21	AA33416 Human PRO212 prote
22	1491	100.0	300	21	AA3621 Human Fas ligand i
23	1491	100.0	300	21	AA97246 M68 TNF receptor r
24	1491	100.0	300	21	AA90357 Human tumour necro
25	1491	100.0	300	21	AA24395 Human PRO212 prote
26	1491	100.0	300	21	AA96596 Human FLINT. Homo
27	1491	100.0	300	22	AAE03568 Human native fas l
28	1491	100.0	300	22	AA74466 Human FLINT native
29	1491	100.0	300	22	AA71754 Human NTR3. Homo
30	1491	100.0	300	22	AA48161 Human PRO212 polyp
31	1491	100.0	300	22	AA50903 Human PRO212 prote
32	1491	100.0	341	22	AA673740 Human colon cancer
33	1487	99.7	271	21	AA19709 Protease-resistant
34	1487	99.7	271	22	AAE03571 Human mature fas l
35	1487	99.7	271	22	AA74467 Human FLINT mature
36	1486	99.7	271	22	AAE03584 Human mature fas l
37	1485	99.6	271	21	AA96599 Human mature FLINT
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DT	17-DEC-1999 (first entry)
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KW	apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW	sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW	reperfusion-associated injury; aplastic anaemia; differentiation;
KW	growth; myelodysplastic syndrome; pancytopenic condition;
KW	myocardial ischaemia.
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OS	Homo sapiens.
XX	
PN	WO950413-A2.
XX	
PD	07-OCT-1999.
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PF	30-MAR-1999; 99WO-US06797.
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PR	30-MAR-1998; 98US-0079856.
PR	20-MAY-1998; 98US-0086074.
PR	09-SEP-1998; 98US-0099643.
PR	17-DEC-1998; 98US-0112577.
PR	18-DEC-1998; 98US-0112703.
PR	22-DEC-1998; 98US-0112933.
PR	22-DEC-1998; 98US-0113407.
XX	
PA	(ELIL ) LILLY & CO ELI.



FT Misc-difference 169 /note= "optionally replaced with Ala"  
 FT Misc-difference 171 /note= "optionally replaced with Asn"  
 FT Misc-difference 172 /note= "optionally replaced with Asn"  
 FT Misc-difference 179 /note= "optionally replaced with Thr"  
 FT Misc-difference 183 /note= "optionally replaced with Lys"  
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 FT Misc-difference 196 /note= "optionally replaced with Thr"  
 FT Misc-difference 209 /note= "optionally replaced with Thr"  
 FT Misc-difference 225 /note= "optionally replaced with Arg"  
 FT Misc-difference 237 /note= "optionally replaced with Glu"  
 FT Misc-difference 270 /note= "optionally replaced with Gly"

WO200058465-A2.

05-OCT-2000.

20-MAR-2000; 2000WO-US06417.

30-MAR-1999; 99US-0126839.

21-JUN-1999; 99US-0140077.

21-JUN-1999; 99US-0140156.

20-OCT-1999; 99US-0160566.

18-FEB-2000; 2000US-0183398.

(ELIL ) LILLY & CO ELI.

Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micanovic R;

Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Witcher DR;

Wroblewski VJ;

WPI; 2000-656167/63.

N-PSDB; AAA75999.

FAS Ligand Inhibitory Protein analogs useful for treating abnormal apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis, chronic obstructive pulmonary disease ulcerative colitis or Crohn's disease

Claim 1; Page 112-113; 114pp; English.

The present sequence represents a mature human FAS Ligand Inhibitory Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature FLINT protein is modified to produce analogues, which have greater potency, longer in vivo half-lives, decreased aggregation, decreased absorption onto surfaces, increased solubility and improved ease of formulation. The FLINT analogue is useful for treating a patient suffering from disease or condition relating to abnormal apoptosis such as acute lung injury, acute respiratory distress syndrome, pulmonary fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or Crohn's disease.

Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 21; Length 271;  
 Best Local Similarity 100.0%; Pred. NO. 4.6e-115;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ||||| 61 ycnvlgereeeerachathnracrtgffahagfclehascppgagviapgtpsqntq 120  
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 QY 121 COPCPGCTESASSSSFOCPHNCNTALGLANVPGSSSHDTICTCTGFPPLSTRVPGAE 180  
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 Db 121 cpcpgptfsassssseqcqhncntalglanvp gssshdtictctgfpplstrvpgae 180  
 QY 181 ECERAVIDFVAFQDISIKRLQRLQALEAPGEGWGPTRAGRAALQKLRRRLTELLCAQD 240  
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 Db 181 eceravidfvafqdisikrlqrlqaleap egwgp tragraalqklrrrltellcaqd 240  
 QY 241 GALLVRLQALRVARMPGLERSVRERPLPVH 271  
 ||||| 241 gallvrlqalrvarmpglersvrerflpvh 271  
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 ID AABI9705 standard; Protein; 271 AA.  
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 AC AABI9705;  
 XX  
 DT 05-FEB-2001 (first entry)  
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 DE Human FAS ligand inhibitor protein FLINT.  
 XX  
 KW FLINT; FAS ligand inhibitory protein; human; protease resistant;  
 KW acute lung injury; acute respiratory distress syndrome;  
 KW chronic obstructive pulmonary disease; pulmonary fibrosis;  
 KW ulcerative colitis; therapy; organ transplantation.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
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 FT Claims 10, 11, 13 and 14"  
 FT Misc-difference 36 /note= "optionally replaced by Thr, as given in  
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 FT Misc-difference 132 /note= "optionally replaced by Asn, as given in  
 FT Claim 12"  
 FT Misc-difference 194 /note= "optionally replaced by Asn, as given in  
 FT Claims 11 and 14"  
 FT Misc-difference 196 /note= "optionally replaced by Thr, as given in  
 FT Claims 11 and 14"  
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 FT occurring amino acid"  
 FT Misc-difference 215 /note= "optionally replaced by any naturally  
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 FT given in Claims 9 and 15"  
 FT Misc-difference 217 /note= "optionally replaced by any naturally  
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 FT given in Claim 9"  
 FT Misc-difference 218 /note= "optionally replaced by any naturally  
 FT occurring amino acid, preferably Gln, Glu,  
 FT Ala, Gly, Ser, Val, Tyr or Asn as given in  
 FT Claims, 9, 10, 11, 12, especially Gln as  
 FT given in Claims 13, 14, 15, 35 and 36"  
 FT



modulators of M68. Modulators of M68 are useful for treatment of cancer and other diseases associated with abnormal levels of apoptosis including systemic lupus erythematosus, Hashimoto's thyroiditis, Grave's disease, idiopathic myxedema, autoimmune diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis, liver diseases, autoimmune gastritis, ulcerative colitis, glomerulonephritis, pulmonary fibrosis, heart failure, atherosclerosis, aplastic anaemia, myelodysplastic syndromes, osteoporosis, Alzheimer's disease, Parkinson's disease, stroke, and myocardial infarction.

XX Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 21; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-115;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAEPTYPWRDAETGERLVCAQCPCPGTFFVQRCRRDSPPTTCGPPRHYYTQFWNYLERCR 60  
 |||||  
 Db 1 vaetpywrdaetgerlvcaqcpgptffvqrcrrdspttcgpprrhytqfwnylerc 60

QY 61 YCNVLCGEREEERACHATHNRACRGTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 120  
 |||||  
 Db 61 ycnvlgereeeerachathnrcrtgffahagfclehascpagviapgtpsqntq 120

QY 121 CQPCPGTFSASSSSSEQCPHNCRTALGLALNPVSSSHDTICTCTGPPPLSTRVPGAE 180  
 |||||  
 Db 121 cqpcpgtfsasssseqcphnrcrtalglalnvpvssshdtictctgfp1strvpgae 180

QY 181 ECERAVIDFVAFODISIKRLQRLQALEAPEGWGPTPRAGRAALQKLRRRLTELLGAQD 240  
 |||||  
 Db 181 ecearavidfvafqdisikrlqrlqaleapegwptpragraalqklrrrltellgaqd 240

QY 241 GALLVRLQLALRVARMPGLERSVRERFLPVH 271  
 |||||  
 Db 241 gallvrlqalrvarmpglersvrerflpvh 271

RESULT 5  
 AAY96598  
 ID AAY96598 standard; Protein; 271 AA.  
 XX  
 AC- AAY96598;  
 XX  
 DT 26-SEP-2000 (first entry)  
 XX  
 DE Human mature FLINT.  
 XX  
 KW FLINT; osteoprotegerin 3; OPG3; tumour necrosis factor receptor; TNFR; FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic; anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic; anti-inflammatory; antibacterial; immunosuppressive.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200037094-A2.  
 XX  
 PD 29-JUN-2000.  
 XX  
 PF 21-DEC-1999; 99WO-US30734.  
 XX  
 PR 22-DEC-1998; 98US-0113407.  
 PR 30-MAR-1999; 99WO-US06797.  
 PR 20-OCT-1999; 99US-0172239.  
 XX  
 XX (ELIL ) LILLY & CO ELI.  
 XX  
 XX Cohen FU, Posada JA, Wierda D;  
 PI WPI; 2000-475441/41.  
 XX  
 DR N-PSDB; AAY51077.  
 XX

PT Use of mature FLINT for treating e.g. acute respiratory distress syndrome, ulcerative colitis or ischemic injury during organ transplantation

PT

XX Example 8; Fig 3; 125pp; English.

XX Human FLINT (also known as osteoprotegerin 3) is a new tumour necrosis factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas mediated apoptotic and pro-inflammatory activity. mFLINT is useful for treating acute respiratory distress syndrome, treating or inhibiting ulcerative colitis, inhibiting ischemic injury during organ transplantation or for organ preservation during transplantation. mFLINT can also be used to treat acute liver failure, inflammation of the liver, abnormal (hepatocyte) apoptosis, sepsis, disorders associated with inflammation, hepatitis, ischemia, hypercoagulation or reperfusion, damage to a cardiac myocyte resulting from abnormal myocardial ischaemia, Type 1 diabetes, cancer, damage to an innocent bystander tissue induced by a chemotherapeutic or therapeutic irradiation, aplastic anaemias, myelodysplastic syndromes and pancytopenic conditions.

XX Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 21; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-115;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAEPTYPWRDAETGERLVCAQCPCPGTFFVQRCRRDSPPTTCGPPRHYYTQFWNYLERCR 60  
 |||||  
 Db 1 vaetpywrdaetgerlvcaqcpgptffvqrcrrdspttcgpprrhytqfwnylerc 60

QY 61 YCNVLCGEREEERACHATHNRACRGTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 120  
 |||||  
 Db 61 ycnvlgereeeerachathnrcrtgffahagfclehascpagviapgtpsqntq 120

QY 121 CQPCPGTFSASSSSSEQCPHNCRTALGLALNPVSSSHDTICTCTGPPPLSTRVPGAE 180  
 |||||  
 Db 121 cqpcpgtfsasssseqcphnrcrtalglalnvpvssshdtictctgfp1strvpgae 180

QY 181 ECERAVIDFVAFODISIKRLQRLQALEAPEGWGPTPRAGRAALQKLRRRLTELLGAQD 240  
 |||||  
 Db 181 ecearavidfvafqdisikrlqrlqaleapegwptpragraalqklrrrltellgaqd 240

QY 241 GALLVRLQLALRVARMPGLERSVRERFLPVH 271  
 |||||  
 Db 241 gallvrlqalrvarmpglersvrerflpvh 271

RESULT 6  
 AAE03567  
 ID AAE03567 standard; Protein; 271 AA.  
 XX  
 AC AAE03567;  
 XX  
 DT 04-AUG-2001 (first entry)  
 XX  
 DE Human mature fas ligand inhibitory protein (FLINT).  
 XX  
 KW Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI; TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS; acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy; chronic obstructive pulmonary disease; COPD; acute lung injury; goitre; rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis; fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis; chronic renal failure; graft-vs-host disease; cutaneous inflammation; vascular leak syndrome; Helicobacter pylori infection; atherosclerosis; insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease; Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis; Down's syndrome; multiple sclerosis; cytostatic; neurotropic; neuroprotective; vasotropic.  
 KW  
 XX Homo sapiens.  
 OS

XX Key Location/Qualifiers  
FH Modified-site 144  
FT /note= "N-linked glycosylation site"  
FT Modified-site 174  
FT /note= "O-linked glycosylation site"  
FT Modified-site 216  
FT /note= "O-linked glycosylation site"  
FT Cleavage-site 218..219  
FT /note= "Proteolytic cleavage"  
XX WO200142463-A1.  
PN 14-JUN-2001.  
XX 29-NOV-2000; 2000WO-US30166.  
XX 07-DEC-1999; 99US-0169367.  
PR 07-DEC-1999; 99US-0169381.  
PR 07-DEC-1999; 99US-0169412.  
PR 23-MAR-2000; 2000US-0191430.  
XX (ELIL ) LILLY & CO ELI.  
XX Lu J, Witcher DR;  
PI WPI; 2001-381684/40.  
DR N-PSDB; AAD07380.  
XX New FLINT polypeptide for treating and/or preventing acute lung injury,  
PT acute respiratory distress syndrome, ulcerative colitis, and  
PT graft-versus-host disease, comprises O-linked or N-linked  
PT oligosaccharides -  
XX  
XX Example 1; Page 52-53; 60pp; English.  
PS  
XX The present sequence is human mature fas ligand inhibitory protein  
CC (FLINT). FLINT, a homologue of tumour necrosis factor receptor  
CC protein (TNFR), binds fas ligand (FasL) and thereby preventing the  
CC interaction of FasL with fas. FLINT comprising O-linked or N-linked  
CC oligosaccharides is useful for preventing or treating acute lung injury  
CC (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,  
CC chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),  
CC to facilitate organ preservation for transplantation and to inhibit T  
CC lymphocyte activation. FLINT is useful for treating and/or preventing  
CC diseases such as rheumatoid arthritis, fibroproliferative lung disease,  
CC fibrotic lung disease, acute lung injury, human immunodeficiency virus  
CC (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-  
CC host disease, cutaneous inflammation, vascular leak syndrome,  
CC Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent  
CC diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,  
CC Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as  
CC psoriasis, Down's syndrome, and multiple sclerosis.  
XX  
SQ Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 22; Length 271;  
Best Local Similarity 100.0%; Pred. No. 4.6e-115;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPGCTFFVORPCRRDSPTTCGPPRHYTQFWNYLERCR 60  
DB 1 vaetptyprdaetgerlvcaqcpptgfvrpcrrdspttcgpprhytqfwnylcr 60  
QY 61 YCNVLGGEREEARACHATHNACRCRTGFFAHAGFCLHASCPCPGAGVIAPGTPSQNTQ 120  
DB 61 ycnvlcgereearachathnacrctrtgffahagfclhascppgagviapgtpsqntq 120  
QY 121 CQCPPTGTFSSSSSEQCPHRNCTALGLALNVPSSSHDTLCTSCGTGFLSTRVPGAE 180  
DB 121 cqcpptgtfssssseqcqhnrnctalglaalnvpssshdtlctscgtgflstrvpgae 180

QY 181 ECERAVIDFAFQDISIKRLQLLQALEAPEGWGPTPRAGRAALQKLRRRLTELIGAQD 240  
DB 181 eceravidfvaqdisikrlqllqaleapegwptpragraalqklrrrltelligaq 240  
QY 241 GALLYVRLLOALVARMPGLERSVRERFLPVH 271  
DB 241 gallvlllqalrvarmpglersvrerflpvh 271  
RESULT 7  
AAB68044  
ID AAB68044 standard; Protein; 271 AA.  
XX  
XX AAB68044;  
XX 29-JUN-2001 (first entry)  
XX  
XX Amino acid sequence of a human mature FLINT polypeptide.  
XX FLINT; Fas ligand inhibitory protein; divalent metal cation; Fas;  
KW Fas ligand; acute liver failure; cerebral ischemia; apoptosis.  
XX Homo sapiens.  
XX OS  
XX WO200118055-A1.  
PN 15-MAR-2001.  
XX  
XX 31-AUG-2000; 2000WO-US20807.  
XX 10-SEP-1999; 99US-0153339.  
PR (ELIL ) LILLY & CO ELI.  
XX  
XX Atkinson PR, Tian Y, Witcher DR;  
XX WPI; 2001-273382/28.  
DR  
XX Compositions comprising a divalent metal cation and a Fas Ligand  
PT Inhibitory protein (FLINT), for reducing or inducing aggregation of  
PT FLINT and for treating diseases involving FasL/Fas and/or  
PT LIGHT/TF-beta-R receptor interactions -  
XX  
XX Example 1; Page 39-40; 44pp; English.  
PS  
XX The present sequence represents a mature FLINT (Fas Ligand Inhibitory  
CC Protein) polypeptide. The specification describes a composition  
CC comprising a divalent metal cation and FLINT protein. The composition  
CC is used either for reducing, reversing or eliminating aggregation and  
CC precipitation of FLINT or for inducing oligomerisation or aggregation  
CC of FLINT molecules. They can be used for purifying FLINT and/or  
CC maintaining FLINT in solution. The compositions are used to treat  
CC and/or prevent disorders associated with the binding of Fas to FasL  
CC and/or LIGHT to the ltbeta and/or TR2/HVEM receptors. Uses include the  
CC treatment of acute liver failure and cerebral ischemia and the prevention  
CC of apoptosis.  
XX  
SQ Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 22; Length 271;  
Best Local Similarity 100.0%; Pred. No. 4.6e-115;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPGCTFFVORPCRRDSPTTCGPPRHYTQFWNYLERCR 60  
DB 1 vaetptyprdaetgerlvcaqcpptgfvrpcrrdspttcgpprhytqfwnylcr 60  
QY 61 YCNVLGGEREEARACHATHNACRCRTGFFAHAGFCLHASCPCPGAGVIAPGTPSQNTQ 120  
DB 61 ycnvlcgereearachathnacrctrtgffahagfclhascppgagviapgtpsqntq 120  
QY 121 CQCPPTGTFSSSSSEQCPHRNCTALGLALNVPSSSHDTLCTSCGTGFLSTRVPGAE 180



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Db 121 cpcpbgtsfssssseqcphnctalglnvpgssshdtlctctgfpplstrvpgae 180
QY 181 ECERAVIDFAVDISIKRLQRLQALEAPEGWPTPRAGRAALQKLRRRLTELLGAQD 240
Db 181 eceravidfvaqdisikrlqrlqaleapegwptpragraalqklrrrltellgaqd 240
QY 241 GALLVRLQALRVARMPLGLSRRERFLPVH 271
Db 241 gallvrlqalrvarmplglersvrerflpvh 271

RESULT 8
AAB68047
ID AAB68047 standard; Protein; 271 AA.
XX
AC AAB68047;
DT 29-JUN-2001 (first entry)
DE Amino acid sequence of a human mature FLINT polypeptide.
XX
KW FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;
KW Fas ligand; acute liver failure; cerebral ischemia; apoptosis.
XX
OS Homo sapiens.
XX
PN WO200118041-A2.
XX
PD 15-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-US20805.
XX
PR 10-SEP-1999; 99US-0153445.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Atkinson PR, Tian Y, Witcher DR;
XX
DR WPI; 2001-273381/28.
XX
CC Compositions comprising a divalent metal cation and a FAS Ligand
PT Inhibitory Protein (FLINT), for reducing or inducing aggregation of
PT FLINT and for treating diseases involving FasL/Fas and/or
PT LIGHT/LT-beta-R receptor interactions -
XX
PS Disclosure; Page 30-31; 33pp; English.
XX
CC The present sequence represents a human mature FLINT (FAS Ligand
CC Inhibitory Protein) polypeptide. The specification describes a
CC composition comprising a divalent metal cation and FLINT protein. The
CC aggregation is used either for reducing, reversing or eliminating
CC aggregation and precipitation of FLINT or for inducing oligomerisation
CC or aggregation of FLINT molecules. They can be used for purifying FLINT
CC and/or maintaining FLINT in solution. The compositions are used to treat
CC and/or prevent disorders associated with the binding of Fas to FasL
CC and/or LIGHT to the LTbetar and/or TR2/HVEM receptors. Uses include the
CC treatment of acute liver failure and cerebral ischemia and the prevention
CC of apoptosis.
XX
SQ Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 22; Length 271;
Best Local Similarity 100.0%; Pred. No. 4.6e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPRDAETGERLVCAQCPGCTFVQRCRRDSPPTCGPCPPRHVTOFNNYLERCR 60
Db 1 vaetptyprdaetgerlvcaqcpptfvgprcrrdsptcgcpprhytqfwnylcr 60
QY 61 YCNVLGGEREEARACHATHNRACRGTGFFAHAGFCLEHASCPCPGAGVIAPGTPSQNTQ 120
Db 61 ycnvlgerereearachathnrcrctgffahagfclehascpagviapgtpsqntq 120
QY 121 CQPCPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTCTGFPPLSTRVPGAE 180

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Db 61 ycnvlgerereearachathnrcrctgffahagfclehascpagviapgtpsqntq 120
QY 121 CQPCPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTCTGFPPLSTRVPGAE 180
Db 121 cpcpbgtsfssssseqcphnctalglnvpgssshdtlctctgfpplstrvpgae 180
QY 181 ECERAVIDFAVDISIKRLQRLQALEAPEGWPTPRAGRAALQKLRRRLTELLGAQD 240
Db 181 eceravidfvaqdisikrlqrlqaleapegwptpragraalqklrrrltellgaqd 240
QY 241 GALLVRLQALRVARMPLGLSRRERFLPVH 271
Db 241 gallvrlqalrvarmplglersvrerflpvh 271

RESULT 9
AAB74465
ID AAB74465 standard; protein; 271 AA.
XX
AC AAB74465;
DT 30-MAY-2001 (first entry)
DE Human FLINT mature protein.
XX
KW Human; FLINT; FAS ligand inhibitory protein; analogue; apoptosis;
KW inflammatory disease.
XX
OS Homo sapiens.
XX
PN WO200118202-A2.
XX
PD 15-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-US20806.
XX
PR 10-SEP-1999; 99US-0153433.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Atkinson PR, Tian Y, Witcher DR;
XX
DR WPI; 2001-257796/26.
XX
PT Compositions useful for reducing/inducing aggregation of a FLINT analog
PT comprise a divalent metal cation and a protease-resistant FAS Ligand
PT Inhibitory Protein (FLINT) analog -
XX
PS Claim 4; Page 41-42; 44pp; English.
XX
CC The present invention describes a composition comprising a divalent metal
CC cation associated with a protease resistant Fas ligand inhibitory protein
CC (FLINT) analogue. The composition is useful in the treatment of diseases
CC associated with Fas binding to its ligand, such as acute liver failure,
CC inflammatory diseases, cerebral ischaemia and apoptosis. The present
CC sequence is the mature FLINT protein.
XX
SQ Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 22; Length 271;
Best Local Similarity 100.0%; Pred. No. 4.6e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPRDAETGERLVCAQCPGCTFVQRCRRDSPPTCGPCPPRHVTOFNNYLERCR 60
Db 1 vaetptyprdaetgerlvcaqcpptfvgprcrrdsptcgcpprhytqfwnylcr 60
QY 61 YCNVLGGEREEARACHATHNRACRGTGFFAHAGFCLEHASCPCPGAGVIAPGTPSQNTQ 120
Db 61 ycnvlgerereearachathnrcrctgffahagfclehascpagviapgtpsqntq 120
QY 121 CQPCPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTCTGFPPLSTRVPGAE 180

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Db 121 cqcpgptfssssseqcqhnrctalglnvpgssshdtlctctgfpplstrvpgae 180
QY 181 ECERAVIDFVAQDISIKRLQLLQALEAPEGWGPTPRAGRAALQKLRRRLTELLGAQD 240
Db 181 eceravidfvaqdisikrlqlqaleapegwptpragraalqklrrrltellgaqd 240
QY 241 GALLVRLQALVARMPGLRSVRERFLPVH 271
Db 241 gallvrlqalvarmpgliersvrerflpvh 271

RESULT 10
ID AAW66102 standard; Protein; 300 AA.
XX
AC AAW66102;
XX
DT 02-DEC-1998 (first entry)
XX
DE Amino acid sequence of tumour necrosis related receptor (TR4).
XX
KW Human; tumour necrosis related receptor; TR4; agonist; antagonist;
KW inhibition; chronic; acute; inflammation; arthritis; septicaemia;
KW autoimmune disease; transplant rejection; stroke; cancer;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN EP861850-A1.
XX
PD 02-SEP-1998.
XX
PF 20-JAN-1998; 98EP-0300382.
XX
PR 04-FEB-1997; 97US-0794796.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Emery J, Tan KB, Truneh A, Young PR;
XX
DR WPI; 1998-508248/44.
XX
DR N-PSDB; AAV07654.
XX
New DNA encoding tumour necrosis related receptor - used to treat
PT and prevent e.g. inflammation, arthritis, septicaemia, autoimmune
PT diseases, transplant rejection, infection, stroke, ischaemia, ARDS,
PT restenosis, AIDS, bone disorders and cancer
XX
PS Claim 1; Fig 1; 21pp; English.
XX
This is the amino acid sequence of the human tumour necrosis related
CC receptor (TR4), used in the method of the invention. The TR4 protein
CC or its agonist can be used to treat a subject in need of enhanced
CC TR4 polypeptide activity. The antagonist is used to inhibit TR4
CC polypeptide activity. The active agents can be used for the
CC treatment and prevention of diseases such as chronic and acute
CC inflammation, arthritis, septicaemia, autoimmune diseases, transplant
CC rejection, stroke, cancer, Alzheimer's disease.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1491; DB 19; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.2e-115;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAEPTYPRDAETGERLVCAQCPTGFVORPCRRDSPTTCGCPPRHYTQFWNYLERCR 60
Db 30 vaetpyprwdaetgerlvcaqcpgptfvrpcrrdspttcgcpprhytqfwnylercr 89
QY 61 YCNVLGGEREEARACHATHNRACRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 120
XX

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Db 90 ycnvlgcereeeearachathnracrtgffahagfclehascpvgagviapgtpsqntg 149
QY 121 COPCPPTFTSASSSSSEQCPHRNCTALGIALNVPGSSSHDTLCTCTGFPPLSTRVPGAE 180
Db 150 cqcpgptfssssseqcqhnrctalglnvpgssshdtlctctgfpplstrvpgae 209
QY 181 ECERAVIDFVAQDISIKRLQLLQALEAPEGWGPTPRAGRAALQKLRRRLTELLGAQD 240
Db 210 eceravidfvaqdisikrlqlqaleapegwptpragraalqklrrrltellgaqd 269
QY 241 GALLVRLQALVARMPGLRSVRERFLPVH 271
Db 270 gallvrlqalvarmpgliersvrerflpvh 300

RESULT 11
AAW63622
ID AAW63622 standard; Protein; 300 AA.
XX
AC AAW63622;
XX
DT 26-OCT-1998 (first entry)
XX
DE Human tumour necrosis factor receptor-6 alpha protein.
XX
KW Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
KW endothelial cells; keratinocytes; normal prostate; apoptosis;
KW prostate tumour tissue.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Protein 31..300
FT Region /note= "TNFR-6 alpha"
FT /note= "Soluble extracellular domain"
XX
PN WO9830694-A2.
XX
PD 16-JUL-1998.
XX
PF 13-JAN-1998; 98WO-US00153.
XX
PR 14-JAN-1997; 97US-0035496.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;
XX
DR WPI; 1998-399142/34.
DR N-PSDB; AAV39085.
XX
Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
PT the diagnosis of immune system-related disorder(s)
XX
PS Claim 20; Fig 1; 91pp; English.
XX
The present sequence represents the human tumour necrosis factor
CC receptor-6 alpha (TNFR-6 alpha) protein. The invention also provides
CC for the TNFR-6 beta protein (AAW63623). TNFR-6 alpha and TNFR-6 beta
CC are members of the tumour necrosis factor receptor (TNFR) family. TNFRs
CC are expressed in endothelial cells, keratinocytes, normal prostate and
CC prostate tumour tissue. For a number of disorders of these cells,
CC particularly of the immune system, substantially altered (whether
CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta
CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta
CC polypeptides, nucleic acids and antibodies are claimed to be useful in
CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and
CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are
CC also claimed to be useful for identifying ligands which may be useful
CC in the treatment of apoptosis related disorders.
XX

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RESULT 14  
AAY17479  
ID AAY17479 standard; Protein; 300 AA.  
XX  
AC AAY17479;

RESULT 15

AAY06817  
 ID AAY06817 standard; Protein; 300 AA.  
 XX  
 AC AAY06817;  
 XX  
 DT 24-JUN-1999 (first entry)  
 XX  
 DE Human Dcr3 polypeptide.  
 XX  
 KW Dcr3 polypeptide; tumour necrosis factor receptor; TNFR; Fas ligand;  
 KW apoptosis; T cell mediated immune response; allergy; asthma; cancer;  
 KW rheumatoid arthritis; Crohn's disease; guest vs. host disease; human;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9914330-A1.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 18-SEP-1998; 98WO-US19661.  
 XX  
 PR 30-JUL-1998; 98US-0094640.  
 PR 18-SEP-1997; 97US-0059288.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Botstein D, Dodge KH, Goddard A, Gurney AL;  
 PI Kim KJ, Lawrence DA, Pitti R, Roy MA, Tumas DB;  
 PI Wood WI;  
 XX  
 DR WPI: 1999-244032/20.  
 DR N-PSDB; AAX32744.  
 XX  
 PT Dcr3 polypeptide related to tumor necrosis factor receptor  
 XX  
 PS Claim 5; Fig 1; 88pp; English.  
 XX  
 CC This represents a human Dcr3 polypeptide, a homologue of tumour necrosis  
 CC factor receptor (TNFR) polypeptide. Host cells containing a vector  
 CC comprising the Dcr3 nucleic acid can be used for the recombinant  
 CC expression of the protein. Dcr3 binds to Fas ligand, so it (or its  
 CC chimeras) are useful for modulating apoptosis in mammalian cells, also  
 CC other Fas-ligand induced activities, particularly to inhibit T cell  
 CC mediated immune responses, e.g. in treatment of allergy, asthma,  
 CC rheumatoid arthritis, Crohn's disease, guest vs. host disease etc. Dcr3  
 CC may also be used to identify specific binding proteins, potential  
 CC inhibitors. Antibodies against Dcr3 are used to treat cancer,  
 CC specifically of the lung and colon, also in diagnosis and for affinity  
 CC purification of the protein. Detecting mutations in the gene for Dcr3 is  
 CC also used to diagnose cancer, or predisposition to it. Dcr3 nucleic acid  
 CC is useful as hybridization probe to detect genomic or related sequences;  
 CC for chromosome and gene mapping; as source of antisense sequences; for  
 CC expression of recombinant Dcr3 and to generate transgenic animals (for  
 CC development and screening of therapeutic agents), also for in vivo or  
 CC ex vivo gene therapy.  
 XX  
 SQ Sequence 300 AA;  
 Query Match 100.0%; Score 1491; DB 20; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-115;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VAETPTYPWRDAETGERLYCAQCPGTFFVQRCRRDSPPTTCGPPRHYTFQWNYLERCR 60  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 30 vaetptyprdaetgerlyvcaqcpgtffvqrcrrdspttcgpprhytqfwnylercr 89  
 QY 61 YCNVLGGEREEERACHATHNRACRRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 90 ycnvlcgereearachathnrcrctgffahagfclehascpvgaviapgtpsqntq 149  
 QY 121 CQPCPPTFSASSSSSEQCPHRNCTALGLALNVPSSSHDTLCTCTGTFPLSTRVPGAE 180

Db 150 cqcpcpptfsassssseqcqhncctalglnvpssshdtlctctgfpplstrvpgae 209  
 QY 181 ECERAVIDFVAFQDISIKRLQRLQLALEAPEGWGTPPRAGRAALQKLRRRLTELLGAQD 240  
 Db 210 eceravidfvaqdisikrlqrlilqaleapegwptpragraaalqklrrrltellgaqd 269  
 QY 241 GALLVLLQALRVARMPGLETSVRERFLPVH 271  
 Db 270 gallvrlilgalrvarmpgliersvrerflpvh 300  
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 Job time: 79 sec

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